



(11) **EP 3 666 901 A1**

(12) **EUROPEAN PATENT APPLICATION**

(43) Date of publication:
17.06.2020 Bulletin 2020/25

(51) Int Cl.:
C12Q 1/37 (2006.01) G01N 33/542 (2006.01)

(21) Application number: **19200945.4**

(22) Date of filing: **27.10.2016**

(84) Designated Contracting States:
**AL AT BE BG CH CY CZ DE DK EE ES FI FR GB
GR HR HU IE IS IT LI LT LU LV MC MK MT NL NO
PL PT RO RS SE SI SK SM TR**

- **JIA, Xiaoqing**
Shanghai, 200131 (CN)
- **WONG, Pin Yee**
South San Francisco, CA 94080 (US)

(30) Priority: **30.10.2015 US 201562249073 P**
04.11.2015 US 201562250885 P

(74) Representative: **Buser, Andres et al**
F. Hoffmann-La Roche AG
Patent Department
Grenzacherstrasse 124
4070 Basel (CH)

(62) Document number(s) of the earlier application(s) in
accordance with Art. 76 EPC:
16801625.1 / 3 368 682

Remarks:

(71) Applicant: **F. Hoffmann-La Roche AG**
4070 Basel (CH)

- The complete document including Reference Tables and the Sequence Listing can be downloaded from the EPO website
- This application was filed on 02.10.2019 as a divisional application to the application mentioned under INID code 62.
- Claims filed after the date of receipt of the divisional application (Rule 68(4) EPC).

(72) Inventors:

- **ORREN, Linda**
Half Moon Bay, CA 94019 (US)
- **MILLER, Aaron**
South San Francisco, CA 94080 (US)

(54) **METHODS OF MEASURING FACTOR D ACTIVITY AND POTENCY OF FACTOR D INHIBITORS**

(57) The invention relates to methods of measuring the activity of Factor D, the key driver in the activation of the alternative complement pathway, methods of determining the potency of Factor D inhibitors, and methods of screening for Factor D inhibitors.

EP 3 666 901 A1

Description**CROSS-REFERENCE TO RELATED APPLICATIONS**

- 5 **[0001]** This application claims the benefit of U.S. Provisional Application Nos. 62/249,073, filed on October 30, 2015, and 62/250,885, filed November 4, 2015, which are incorporated by reference herein in their entireties.

REFERENCE TO SEQUENCE LISTING SUBMITTED ELECTRONICALLY

- 10 **[0002]** This application incorporates by reference a Sequence Listing submitted with this application as a text file entitled "12279-705-228_SEQLIST.txt" created on October 19, 2016 and having a size of 1,647,578 bytes.

1. FIELD

- 15 **[0003]** The invention relates to methods of measuring the activity of Factor D, the key driver in the activation of the alternative complement pathway, methods of determining the potency of Factor D inhibitors, and methods of screening for Factor D inhibitors.

2. BACKGROUND

- 20 **[0004]** Factor D is a highly specific chymotrypsin like serine protease that is a rate limiting enzyme in the activation of the complement alternative pathway (Katsche et al., 2012, J Biol Chem 287:12886-12892). Increased activation of the alternative complement pathway has been found in drusen, cytotoxic deposits present on the Bruch's membrane, which are associated with the development of age related macular degeneration (AMD) (Damico et al., 2012, Arq Bras Oftalmol 75:71-75).

25 **[0005]** Inhibitors of Factor D are being developed as therapeutics to prevent activation of the alternative complement pathway, thereby inhibiting inflammation and cytotoxic activity of the activated complement components (Tanhehco, 1999, Transplant Proc 31:2168-2171).

- 30 **[0006]** Activation of the alternative complement pathway is typically measured by adding human serum to rabbit erythrocytes. Next, intact erythrocytes and cellular debris are pelleted by centrifugation and lysis is determined by measuring the absorbance at 412 nm arising from the release of hemoglobin into the supernatant.

35 **[0007]** Citation of a reference herein shall not be construed as an admission that such is prior art to the present disclosure.

3. SUMMARY OF THE INVENTION

- 40 **[0008]** The invention relates to methods of measuring Factor D activity, methods of determining the potency of Factor D inhibitors, and methods of screening for Factor D inhibitors, all of which comprise measuring Factor B cleavage using a proximity-based measurement assay. The methods are simple, fast, homogeneous and adaptable to high-throughput assays, and are based in part on the inventors' development and characterization of an assay that measures the ability of lampalizumab (an anti-Factor D antibody) to inhibit the enzymatic activity of Factor D (see Section 6). The substrate for Factor D is another alternative complement pathway serine protease, Factor B. Factor C3b binds to Factor B; then, Factor D cleaves Factor B into Factor Ba and Factor Bb. Factor Bb remains bound to Factor C3b, forming the active C3 convertase, which initiates the alternative complement pathway (Volanakis, et al., 1996, Protein Science 5:553-564).
- 45 Therefore, if Factor B is not cleaved by Factor D, Factor Ba and Factor Bb will be in spatial proximity with each other, Factor C3b and Factor Ba will also be in spatial proximity with each other. When Factor B is cleaved by Factor D, however, Factor Ba and Factor Bb will be apart from each other, and Factor C3b and Factor Ba will also be apart from each other.

- 50 **[0009]** In certain embodiments, the methods described herein rely on the distance between Factor Ba and Factor Bb, wherein one of the two is labeled with a donor, and the other is labeled with an acceptor. In such embodiments, the donor and/or the acceptor may be attached to Factor Ba or Factor Bb, respectively, by a protein (e.g., an antibody or antigen-binding fragment thereof), peptide, peptide mimetic, aptamer, nucleotide (e.g., DNA, RNA, shRNA, miRNA, siRNA, antisense DNA), or any other molecule that binds to Factor Ba or Factor Bb, or by direct chemical labeling (when the donor is attached to Factor Ba, the acceptor is attached to Factor Bb; when the donor is attached to Factor Bb, the acceptor is attached to Factor Ba).

55 **[0010]** In certain embodiments, the methods described herein rely on the distance between Factor C3b and Factor Ba, wherein one of the two is labeled with a donor, and the other is labeled with an acceptor. In such embodiments, the donor and/or the acceptor may be attached to Factor C3b or Factor Ba, respectively, by a protein (e.g., an antibody or

antigen-binding fragment thereof), peptide, peptide mimetic, aptamer, nucleotide (e.g., DNA, RNA, shRNA, miRNA, siRNA, antisense DNA), or any other molecule that binds to Factor C3b or Factor Ba, or by direct chemical labeling (when the donor is attached to Factor C3b, the acceptor is attached to Factor Ba; when the donor is attached to Factor Ba, the acceptor is attached to Factor C3b).

[0011] To more precisely measure Factor D activity or the potency of Factor D inhibitors, a quencher can be added to terminate the enzymatic cleavage of Factor B by Factor D before measuring. Luckily, the inventors have discovered that when both anti-Factor Ba and anti-Factor Bb are used as detection reagents, they quench the Factor D activity in the assay, therefore obviating the need to add another quencher.

[0012] The methods of measuring Factor D activity are useful, for example, in diagnosing or staging a human patient having or suspected of having a disorder associated with increased or decreased Factor D activity relative to a normal person. The methods of determining the potency of Factor D inhibitors are useful, for example, in assessing the quality of anti-Factor D therapeutics for quality control in batch manufacturing, and in testing the potency of selected anti-Factor D therapeutic leads. The methods of screening for Factor D inhibitors are useful, for example, in high-throughput screening for new Factor D inhibitors.

[0013] In one aspect, provided herein are methods of measuring the activity of Factor D in a sample derived from a subject (e.g., a human), comprising performing a proximity-based measurement assay, wherein the proximity-based measurement assay measures the cleavage of Factor B.

[0014] In various embodiments, the methods of measuring the activity of Factor D comprise (a) adding to the sample an anti-Factor Ba antibody labeled with a first moiety and an anti-Factor Bb antibody labeled with a second moiety, wherein one of the moieties is a donor, and the other moiety is an acceptor, and wherein a proximity signal generated by the acceptor and/or the donor indicates that Factor Ba and Factor Bb are in proximity; and (b) measuring the value of the proximity signal from the sample; wherein the activity of Factor D in the sample is negatively correlated with the value of the proximity signal. In some embodiments, the methods further comprise a step of quenching the activity of Factor D in the sample by providing an excessive amount of a quencher (e.g., a Factor D inhibitor) to the sample before the step of (a).

[0015] In certain aspects of such various embodiments, the methods of measuring the activity of Factor D further comprise: (c) adding to a control sample the anti-Factor Ba antibody labeled with the first moiety and the anti-Factor Bb antibody labeled with the second moiety; and (d) measuring the value of the proximity signal from the control sample; wherein a greater value of the proximity signal from the sample relative to the control sample indicates a lower activity of Factor D in the sample relative to the control sample. In some embodiments, the methods further comprise a step of quenching the activity of Factor D in the sample by providing an excessive amount of a quencher (e.g., a Factor D inhibitor) to the sample before the step of (a), and a step of quenching the activity of Factor D in the control sample by providing an excessive amount of the quencher to the control sample before the step of (c).

[0016] In some embodiments of the methods of measuring the activity of Factor D as described, the anti-Factor Ba antibody and the anti-Factor Bb antibody quench the activity of Factor D.

[0017] In other various embodiments, the methods of measuring the activity of Factor D comprise (a) adding to the sample an anti-Factor C3b antibody labeled with a first moiety and an anti-Factor Ba antibody labeled with a second moiety, wherein one of the moieties is a donor, and the other moiety is an acceptor, and wherein a proximity signal generated by the acceptor and/or the donor indicates that Factor C3b and Factor Ba are in proximity; and (b) measuring the value of the proximity signal from the sample; wherein the activity of Factor D in the sample is negatively correlated with the value of the proximity signal. In some embodiments, the methods further comprise a step of quenching the activity of Factor D in the sample by providing an excessive amount of a quencher (e.g., a Factor D inhibitor) to the sample before the step of (a).

[0018] In certain aspects of such other various embodiments, the methods of measuring the activity of Factor D further comprise: (c) adding to a control sample the anti-Factor C3b antibody labeled with the first moiety and the anti-Factor Ba antibody labeled with the second moiety; and (d) measuring the value of the proximity signal from the control sample; wherein a greater value of the proximity signal from the sample relative to the control sample indicates a lower activity of Factor D in the sample relative to the control sample. In some embodiments, the methods further comprise a step of quenching the activity of Factor D in the sample by providing an excessive amount of a quencher (e.g., a Factor D inhibitor) to the sample before the step of (a), and a step of quenching the activity of Factor D in the control sample by providing an excessive amount of the quencher to the control sample before the step of (c).

[0019] In specific embodiments of the methods of measuring the activity of Factor D described herein, the Factor B is a recombinantly expressed Factor B. In specific embodiments of the methods of measuring the activity of Factor D described herein, the Factor B is endogenously expressed Factor B purified from a sample derived from a subject.

[0020] In another aspect, provided herein are methods of determining the potency of a Factor D inhibitor in inhibiting Factor D activity, comprising performing a proximity-based measurement assay, wherein the proximity-based measurement assay measures the cleavage of Factor B.

[0021] In various embodiments, the methods of determining the potency of a Factor D inhibitor comprise: (a) mixing

the Factor D inhibitor with Factor D, Factor B and Factor C3b in a test reaction mix; (b) incubating the test reaction mix; (c) adding to the test reaction mix an anti-Factor Ba antibody labeled with a first moiety and an anti-Factor Bb antibody labeled with a second moiety after the step of (b), wherein one of the moieties is a donor, and the other moiety is an acceptor, and wherein a proximity signal generated by the acceptor and/or the donor indicates that Factor Ba and Factor Bb are in proximity; and (d) measuring the value of the proximity signal from the test reaction mix; wherein the potency of the Factor D inhibitor is positively correlated with the value of the proximity signal. In some embodiments, the methods further comprise a step of quenching the activity of Factor D in the sample by providing an excessive amount of a quencher (e.g., a Factor D inhibitor) to the sample before the step of (c).

[0022] In certain aspects of such various embodiments, the methods of determining the potency of a Factor D inhibitor further comprise: (e) mixing a control reaction mix; (f) incubating the control reaction mix; (g) adding to the control reaction mix the anti-Factor Ba antibody labeled with the first moiety and the anti-Factor Bb antibody labeled with the second moiety after the step of (f); and (h) measuring the value of the proximity signal from the control test reaction mix; wherein a greater value of the proximity signal from the test reaction mix relative to the control reaction mix indicates a greater inhibition of Factor D activity by the Factor D inhibitor in the test reaction mix relative to the control reaction mix. In some embodiments, the methods further comprise a step of quenching the activity of Factor D in the sample by providing an excessive amount of a quencher (e.g., a Factor D inhibitor) to the sample before the step of (c), and a step of quenching the activity of Factor D in the control sample by providing an excessive amount of the quencher to the control sample before the step of (g).

[0023] In some embodiments of the methods of determining the potency of a Factor D inhibitor, the anti-Factor Ba antibody and the anti-Factor Bb antibody quench the activity of Factor D.

[0024] In other various embodiments, the methods of determining the potency of a Factor D inhibitor comprise: (a) mixing the Factor D inhibitor with Factor D, Factor B and Factor C3b in a test reaction mix; (b) incubating the test reaction mix; (c) adding to the test reaction mix an anti-Factor C3b antibody labeled with a first moiety and an anti-Factor Ba antibody labeled with a second moiety after the step of (b), wherein one of the moieties is a donor, and the other moiety is an acceptor, and wherein a proximity signal generated by the acceptor and/or the donor indicates that Factor C3b and Factor Ba are in proximity; and (d) measuring the value of the proximity signal from the test reaction mix; wherein the potency of the Factor D inhibitor is positively correlated with the value of the proximity signal. In some embodiments, the methods further comprise a step of quenching the activity of Factor D in the sample by providing an excessive amount of a quencher (e.g., a Factor D inhibitor) to the sample before the step of (c).

[0025] In certain aspects of such other various embodiments, the methods of determining the potency of a Factor D inhibitor further comprise: (e) mixing a control reaction mix; (f) incubating the control reaction mix; (g) adding to the control reaction mix the anti-Factor C3b antibody labeled with the first moiety and the anti-Factor Ba antibody labeled with the second moiety after the step of (f); and (h) measuring the value of the proximity signal from the control test reaction mix; wherein a greater value of the proximity signal from the test reaction mix relative to the control reaction mix indicates a greater inhibition of Factor D activity by the Factor D inhibitor in the test reaction mix relative to the control reaction mix. In some embodiments, the methods further comprise a step of quenching the activity of Factor D in the sample by providing an excessive amount of a quencher (e.g., a Factor D inhibitor) to the sample before the step of (c), and a step of quenching the activity of Factor D in the control sample by providing an excessive amount of the quencher to the control sample before the step of (g).

[0026] In specific embodiments of the methods of determining the potency of a Factor D inhibitor, the Factor D inhibitor is an antibody or an antigen-binding fragment thereof (e.g., lampalizumab).

[0027] In specific embodiments, the antibody comprises one, two, three, four, five or six of the following HVRs: (i) an HVR-H1 comprising the amino acid sequence of SEQ ID NO: 1; (ii) an HVR-H2 comprising the amino acid sequence of SEQ ID NO: 2, SEQ ID NO: 3, or SEQ ID NO: 4; (iii) an HVR-H3 comprising the amino acid sequence of SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, or SEQ ID NO: 8; (iv) an HVR-L1 comprising the amino acid sequence of SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, or SEQ ID NO: 17; (v) an HVR-L2 comprising the amino acid sequence of SEQ ID NO: 18; or (vi) an HVR-L3 comprising the amino acid sequence of SEQ ID NO: 19 or SEQ ID NO: 20.

[0028] In specific embodiments, the antibody comprises one, two, three, four, five or six of the following HVRs: (i) an HVR-H1 comprising the amino acid sequence of SEQ ID NO: 85; (ii) an HVR-H2 comprising the amino acid sequence of SEQ ID NO: 86, SEQ ID NO: 87, SEQ ID NO: 88, SEQ ID NO: 89, SEQ ID NO: 90, SEQ ID NO: 91, SEQ ID NO: 92, SEQ ID NO: 93, or SEQ ID NO: 94; (iii) an HVR-H3 comprising the amino acid sequence of SEQ ID NO: 95; (iv) an HVR-L1 comprising the amino acid sequence of SEQ ID NO: 96; (v) an HVR-L2 comprising the amino acid sequence of SEQ ID NO: 97, SEQ ID NO: 98, or SEQ ID NO: 99; or (vi) an HVR-L3 comprising the amino acid sequence of SEQ ID NO: 100 or SEQ ID NO: 101.

[0029] In specific embodiments of the methods of determining the potency of a Factor D inhibitor described herein, the Factor D is a recombinantly expressed Factor D. In specific embodiments of the methods of determining the potency of a Factor D inhibitor described herein, the Factor D is endogenously expressed Factor D purified from a sample derived

from a subject.

[0030] In specific embodiments of the methods of determining the potency of a Factor D inhibitor described herein, the Factor B is a recombinantly expressed Factor B. In specific embodiments of the methods of determining the potency of a Factor D inhibitor described herein, the Factor B is endogenously expressed Factor B purified from a sample derived from a subject.

[0031] In another aspect, provided herein are methods of screening for a Factor D inhibitor from a plurality of Factor D inhibitor candidates, comprising performing a proximity-based measurement assay, wherein the proximity-based measurement assay measures the cleavage of Factor B.

[0032] In various embodiments, the methods of screening for a Factor D inhibitor comprise: (a) mixing a Factor D inhibitor candidate with Factor D, Factor B and Factor C3b in a test reaction mix; (b) incubating the test reaction mix; (c) adding to the test reaction mix an anti-Factor Ba antibody labeled with a first moiety and an anti-Factor Bb antibody labeled with a second moiety after the step of (b), wherein one of the moieties is a donor, and the other is an acceptor, and wherein a proximity signal generated by the acceptor and/or the donor indicates that Factor Ba and Factor Bb are in proximity; and (d) measuring the value of the proximity signal from the test reaction mix; wherein the degree of Factor D activity inhibition by a Factor D candidate is positively correlated with the value of the proximity signal. In some embodiments, the methods further comprise a step of quenching the activity of Factor D in the sample by providing an excessive amount of a quencher (e.g., a Factor D inhibitor) to the sample before the step of (c).

[0033] In certain aspects of such various embodiments, the methods of screening for a Factor D inhibitor further comprise: (e) mixing a control reaction mix; (f) incubating the control reaction mix; (g) adding to the control reaction mix the anti-Factor Ba antibody labeled with the first moiety and the anti-Factor Bb antibody labeled with the second moiety after the step of (f); and (h) measuring the value of the proximity signal from the control test reaction mix; wherein a greater value of the proximity signal from the test reaction mix relative to the control reaction mix indicates a greater inhibition of Factor D activity by the Factor D inhibitor candidate in the test reaction mix relative to the control reaction mix. In some embodiments, the methods further comprise a step of quenching the activity of Factor D in the sample by providing an excessive amount of a quencher to the sample before the step of (c), and a step of quenching the activity of Factor D in the control sample by providing an excessive amount of the quencher (e.g., a Factor D inhibitor) to the control sample before the step of (g).

[0034] In some embodiments of the methods of screening for a Factor D inhibitor, the anti-Factor Ba antibody and the anti-Factor Bb antibody quench the activity of Factor D.

[0035] In other various embodiments, the methods of screening for a Factor D inhibitor comprise: (a) mixing a Factor D inhibitor candidate with Factor D, Factor B and Factor C3b in a test reaction mix; (b) incubating the test reaction mix; (c) adding to the test reaction mix an anti-Factor C3b antibody labeled with a first moiety and an anti-Factor Ba antibody labeled with a second moiety after the step of (b), wherein one of the moieties is a donor, and the other is an acceptor, and wherein a proximity signal generated by the acceptor and/or the donor indicates that Factor C3b and Factor Ba are in proximity; and (d) measuring the value of the proximity signal from the test reaction mix; wherein the degree of Factor D activity inhibition by a Factor D candidate is positively correlated with the value of the proximity signal. In some embodiments, the methods further comprise a step of quenching the activity of Factor D in the sample by providing an excessive amount of a quencher (e.g., a Factor D inhibitor) to the sample before the step of (c).

[0036] In certain aspects of such other various embodiments, the methods of screening for a Factor D inhibitor further comprise: (e) mixing a control reaction mix; (f) incubating the control reaction mix; (g) adding to the control reaction mix the anti-Factor C3b antibody labeled with the first moiety and the anti-Factor Ba antibody labeled with the second moiety after the step of (f); and (h) measuring the value of the proximity signal from the control test reaction mix; wherein a greater value of the proximity signal from the test reaction mix relative to the control reaction mix indicates a greater inhibition of Factor D activity by the Factor D inhibitor candidate in the test reaction mix relative to the control reaction mix. In some embodiments, the methods further comprise a step of quenching the activity of Factor D in the sample by providing an excessive amount of a quencher to the sample before the step of (c), and a step of quenching the activity of Factor D in the control sample by providing an excessive amount of the quencher (e.g., a Factor D inhibitor) to the control sample before the step of (g).

[0037] In specific embodiments of the methods of screening for a Factor D inhibitor, the steps of (a)-(d) are carried out for each Factor D inhibitor candidate from the plurality.

[0038] In specific embodiments of the methods of screening for a Factor D inhibitor, the proximity-based measurement assay is carried out in a microplate.

[0039] In specific embodiments of the methods of screening for a Factor D inhibitor, the proximity-based measurement assay is conducted in a high-throughput manner.

[0040] In specific embodiments of the methods of screening for a Factor D inhibitor, the Factor D inhibitor candidate is an antibody or an antigen-binding fragment thereof (e.g., lampalizumab).

[0041] When anti-Factor Ba antibody and anti-Factor Bb antibody are used, in some embodiments of the methods described above, the anti-Factor Ba antibody is biotinylated, and the first moiety comprises streptavidin, avidin, or

neutravidin (preferably streptavidin). In other embodiments, the anti-Factor Ba antibody is directly conjugated to the first moiety. In some embodiments, the anti-Factor Bb antibody is biotinylated, and the second moiety comprises streptavidin, avidin, or neutravidin (preferably streptavidin). In other embodiments, the anti-Factor Bb antibody is directly conjugated to the second moiety.

[0042] When anti-Factor C3b antibody and anti-Factor Ba antibody are used, in some embodiments of the methods described above, the anti-Factor C3b antibody is biotinylated, and the first moiety comprises streptavidin, avidin, or neutravidin (preferably streptavidin). In other embodiments, the anti-Factor C3b antibody is directly conjugated to the first moiety. In some embodiments, the anti-Factor Ba antibody is biotinylated, and the second moiety comprises streptavidin, avidin, or neutravidin (preferably streptavidin). In other embodiments, the anti-Factor Ba antibody is directly conjugated to the second moiety.

[0043] In certain embodiments of the methods described above, the donor and/or the acceptor is in the form of beads (e.g., AlphaScreen beads).

[0044] In certain embodiments of the methods described above, the donor comprises Europium, the acceptor comprises Alexa 647, and the light source has a wavelength of about 340 nm.

[0045] In specific embodiments of the methods of screening for a Factor D inhibitor described herein, the Factor D is a recombinantly expressed Factor D. In specific embodiments of the methods of screening for a Factor D inhibitor described herein, the Factor D is endogenously expressed Factor D purified from a sample derived from a subject.

[0046] In specific embodiments of the methods of screening for a Factor D inhibitor described herein, the Factor B is a recombinantly expressed Factor B. In specific embodiments of the methods of screening for a Factor D inhibitor described herein, the Factor B is endogenously expressed Factor B purified from a sample derived from a subject.

[0047] In another aspect, provided herein are kits for measuring Factor D activity, determining Factor D inhibitor potency, and/or screening for Factor D inhibitors.

[0048] In various embodiments, the kits comprise an anti-Factor Ba antibody, an anti-Factor Bb antibody, a first moiety and a second moiety, wherein: (a) the anti-Factor Ba antibody is labeled or can be labeled with the first moiety, the anti-Factor Bb antibody is labeled or can be labeled with the second moiety; and (b) one of the moieties is a donor, and the other moiety is an acceptor.

[0049] In specific embodiments, the anti-Factor Ba antibody and/or the anti-Factor Bb antibody is immobilized on a solid surface. In specific embodiments, the solid surface is a plate, a microplate, a chip, a membrane, or a bead.

[0050] In other various embodiments, the kits comprise an anti-Factor C3b antibody, an anti-Factor Ba antibody, a first moiety and a second moiety, wherein: (a) the anti-Factor C3b antibody is labeled or can be labeled with the first moiety, the anti-Factor Ba antibody is labeled or can be labeled with the second moiety; and (b) one of the moieties is a donor, and the other moiety is an acceptor.

[0051] In specific embodiments, the anti-Factor C3b antibody and/or the anti-Factor Ba antibody is immobilized on a solid surface. In specific embodiments, the solid surface is a plate, a microplate, a chip, a membrane, or a bead.

[0052] In certain embodiments, the kits described herein further comprise a control sample with known Factor D activity.

[0053] In certain embodiments, the kits described herein further comprise a control Factor D inhibitor with known potency of inhibiting Factor D activity.

[0054] In certain embodiments, the kits described herein further comprise a quencher. In specific embodiments, the quencher is a Factor D inhibitor.

[0055] In specific embodiments, the kits described herein further comprise a recombinantly expressed Factor B. In specific embodiments, the kits described herein further comprise an endogenously expressed Factor B purified from a sample derived from a subject.

[0056] In specific embodiments, the kits described herein further comprise a recombinantly expressed Factor D. In specific embodiments, the kits described herein further comprise an endogenously expressed Factor D purified from a sample derived from a subject.

3.1. DEFINITIONS

[0057] The terms used throughout this application are to be construed with ordinary and typical meaning to those of ordinary skill in the art. However, the following definitions are provided in order to facilitate an understanding of the invention.

[0058] The phrase "proximity signal" refers to a signal that is generated by an acceptor and/or a donor when the acceptor and the donor (each of which is part of, binds to, or is attached to one member of a protein pair) are brought to close proximity. The value of the proximity signal is sensitive to the distance between the acceptor and the donor. In some embodiments, the proximity signal is a signal generated by the acceptor and the donor which indicates that the acceptor and the donor (and thus the protein pair) are in proximity. In some embodiments, the proximity signal is a signal generated by the acceptor which indicates that the acceptor and the donor (and thus the protein pair) are in proximity. In some embodiments, the proximity signal is a signal generated by the donor which indicates that the acceptor and the

donor (and thus the protein pair) are in proximity. For example, when the Fluorescence Resonance Energy Transfer (FRET) technology is utilized to assay the distance between the donor and the acceptor, the proximity signal can be the ratio between the FRET acceptor's fluorescence emission intensity and the FRET donor's fluorescence emission intensity that is higher than a baseline level (e.g., about 2-fold, 5-fold, 10-fold, 20-fold, 50-fold, 100-fold higher or more) (a baseline level here is the ratio between the FRET acceptor's fluorescence emission intensity and the FRET donor's fluorescence emission intensity when the FRET acceptor and the FRET donor are apart (e.g., more than 10 nm, 20 nm, 50 nm, 100 nm, or 200 nm apart)). In another example, when the AlphaScreen® technology is utilized to assay the distance between the donor and the acceptor, the proximity signal can be the acceptor's emission intensity that is higher than a baseline level (e.g., about 2-fold, 5-fold, 10-fold, 20-fold, 50-fold, 100-fold higher or more) (a baseline level here is the acceptor's emission intensity when the acceptor and the donor are apart (e.g., more than 200 nm, 300 nm, 400 nm, 500 nm, 1000 nm, 2000 nm apart)).

[0059] The phrase "Factor D activity" or "activity of Factor D" refers to the enzymatic activity of Factor D to cleave Factor B.

[0060] The phrase "Factor D inhibitor" or "inhibitor of Factor D" refers to a pharmaceutical agent that reduces or blocks the activity of Factor D.

[0061] The phrase "positively correlated" is used to describe the relationship between a pair of items that both change in value in the same direction. For example, if A is "positively correlated" with B, the value of A will increase when the value of B increases, and will decrease when the value of B decreases.

[0062] The phrase "negatively correlated" is used to describe the relationship between a pair of items that both change in value in the opposite direction. For example, if A is "negatively correlated" with B, the value of A will decrease when the value of B increases, and will increase when the value of B decreases.

[0063] The term "subject" referred to throughout this application, can be, but is not limited to, a human or non-human vertebrate such as a wild, domestic or farm animal. In certain embodiments, the subject is a mammal, e.g., a human, a cow, a dog, a cat, a goat, a horse, a sheep, a pig, a rat, or a mouse. In a preferred embodiment, the subject is a human. In some embodiments, the subject is a human patient having or suspected of having a disorder associated with increased or decreased Factor D activity relative to a normal person.

[0064] The term "quench" with respect to the activity of Factor D means to terminate the enzymatic cleavage of Factor B by Factor D.

[0065] The term "quencher" refers to an agent capable of terminating the enzymatic cleavage of Factor B by Factor D.

[0066] The term "antibody" is used in the broadest sense, and specifically covers full length monoclonal antibodies, polyclonal antibodies, multispecific antibodies (e.g., bispecific antibodies) and antibody fragments so long as they exhibit the desired biological activity such as antigen-binding activity. Antibodies (Abs) and immunoglobulins (Igs) are glycoproteins having the same structural characteristics. While antibodies exhibit binding specificity to a specific target, immunoglobulins include both antibodies and other antibody-like molecules which lack target specificity. Native antibodies and immunoglobulins are usually heterotetrameric glycoproteins of about 150,000 daltons, composed of two identical light (L) chains and two identical heavy (H) chains. Each heavy chain has at one end a variable domain (V_H) followed by a number of constant domains. Each light chain has a variable domain at one end (V_L) and a constant domain at its other end. The term "Antibody" as used herein expressly encompasses antibody fragments retaining antigen-binding activity.

[0067] An "antibody fragment" refers to a molecule other than an intact antibody that comprises a portion of an intact antibody that binds the antigen to which the intact antibody binds. Examples of antibody fragments include but are not limited to Fv, Fab, Fab', Fab-SH, Fab'-SH, Fab-C, Fab'-C, Fab-C-SH, Fab'-C-SH, F(ab')₂; diabodies; linear antibodies; single-chain antibody molecules (e.g., scFv); and multispecific antibodies formed from antibody fragments.

[0068] As used herein, a "Fab" refers to an antibody that comprises a heavy chain constant region that comprises the CH1 domain, or a sufficient portion of the CH1 domain to form a disulfide bond with the light chain constant region, but does not contain a CH2 domain or a CH3 domain. As used herein, a Fab may comprise one or more amino acids of the hinge region. Thus, as used herein, the term "Fab" encompasses Fab' antibodies. A Fab may comprise additional non-native amino acids, such as a C-terminal cysteine, in which case it may be referred to as a Fab-C. As discussed below, the term Fab-C also encompasses Fabs comprising native amino acids of the hinge region, including a native cysteine at the C-terminus. In some embodiments, a Fab comprises an engineered cysteine (i.e., a Fab may be a THIOMAB).

[0069] A "Fab-C" refers to a Fab with a C-terminal cysteine, which may be a native cysteine that occurs at that residue position (such as a cysteine from the hinge region), or may be a cysteine added to the C-terminus that does not correspond to a native cysteine. Nonlimiting exemplary Fab-C heavy chain constant regions include the sequences of SEQ ID NOs: 863, 875, and 876.

[0070] A "Fab-SH" refers to a Fab with a free thiol group. In some embodiments, the free thiol group is located in the last 10 amino acids of the C-terminus of the Fab. Fab-C antibodies are typically also Fab-SH antibodies. A further nonlimiting exemplary Fab-SH heavy chain constant region having the amino acid sequence of SEQ ID NO: 865. Typically, a Fab comprising an engineered cysteine (i.e., a Fab that is a THIOMAB) is a Fab-SH.

[0071] The term "variable region" or "variable domain" refers to the domain of an antibody heavy or light chain that is involved in binding the antibody to antigen. The variable domains of the heavy chain and light chain (VH and VL, respectively) of a native antibody generally have similar structures, with each domain comprising four conserved framework regions (FRs) and three hypervariable regions (HVRs). (See, e.g., Kindt et al. *Kuby Immunology*, 6th ed., W.H. Freeman and Co., page 91 (2007).) A single VH or VL domain may be sufficient to confer antigen-binding specificity. Furthermore, antibodies that bind a particular antigen may be isolated using a VH or VL domain from an antibody that binds the antigen to screen a library of complementary VL or VH domains, respectively. See, e.g., Portolano et al., *J. Immunol.* 150:880-887 (1993); Clarkson et al., *Nature* 352:624-628 (1991).

[0072] The term "variable" refers to the fact that certain portions of the variable domains differ extensively in sequence among antibodies and are used in the binding and specificity of each particular antibody for its particular antigen. However, the variability is not evenly distributed throughout the variable domains of antibodies. It is concentrated in three segments called hypervariable regions both in the light chain and the heavy chain variable domains. The more highly conserved portions of variable domains are called the framework regions (FRs). The variable domains of native heavy and light chains each comprise four FRs, largely adopting a β -sheet configuration, connected by three hypervariable regions, which form loops connecting, and in some cases forming part of, the β -sheet structure. The hypervariable regions in each chain are held together in close proximity by the FRs and, with the hypervariable regions from the other chain, contribute to the formation of the antigen-binding site of antibodies (see Kabat et al., *Sequences of Proteins of Immunological Interest*, 5th Ed. Public Health Service, National Institutes of Health, Bethesda, Md. (1991)). The constant domains are not involved directly in binding an antibody to an antigen, but exhibit various effector functions, such as participation of the antibody in antibody dependent cellular cytotoxicity (ADCC).

[0073] Papain digestion of antibodies produces two identical antigen-binding fragments, called "Fab" fragments, each with a single antigen-binding site, and a residual "Fc" fragment, whose name reflects its ability to crystallize readily. Pepsin treatment yields an F(ab')₂ fragment that has two antigen-binding sites and is still capable of cross-linking antigen.

[0074] The Fab fragment also contains the constant domain of the light chain and the first constant domain (CH1) of the heavy chain. Fab' fragments differ from Fab fragments by the addition of a few residues at the carboxy terminus of the heavy chain CH1 domain including one or more cysteines from the antibody hinge region. Fab'-SH is the designation herein for Fab' in which the cysteine residue(s) of the constant domains bear at least one free thiol group. F(ab')₂ antibody fragments originally were produced as pairs of Fab' fragments which have hinge cysteines between them. Other chemical couplings of antibody fragments are also known.

[0075] "Fv" is the minimum antibody fragment which contains a complete antigen-recognition and antigen-binding site. This region consists of a dimer of one heavy chain and one light chain variable domain in tight, non-covalent association. It is in this configuration that the three hypervariable regions of each variable domain interact to define an antigen-binding site on the surface of the VH-VL dimer. Collectively, the six hypervariable regions confer antigen-binding specificity to the antibody. However, even a single variable domain (or half of an Fv comprising only three hypervariable regions specific for an antigen) has the ability to recognize and bind antigen, although at a lower affinity than the entire binding site.

[0076] The term "hypervariable region" or "HVR," as used herein, refers to each of the regions of an antibody variable domain which are hypervariable in sequence and/or form structurally defined loops ("hypervariable loops"). Generally, native four-chain antibodies comprise six HVRs; three in the VH (H1, H2, H3), and three in the VL (L1, L2, L3). HVRs generally comprise amino acid residues from the hypervariable loops and/or from the "complementarity determining regions" (CDRs), the latter being of highest sequence variability and/or involved in antigen recognition. HVR-H3 is believed to play a unique role in conferring fine specificity to antibodies. See, e.g., Xu et al. (2000) *Immunity* 13:37-45; Johnson and Wu (2003) in *Methods in Molecular Biology* 248:1-25 (Lo, ed., Human Press, Totowa, N.J.). "Framework Region" or "FR" residues are those variable domain residues other than the hypervariable region residues as herein defined. An HVR region as used herein comprise any number of residues located within positions 24-36 (for L1), 46-56 (for L2), 89-97 (for L3), 26-35B (for H1), 47-65 (for H2), and 93-102 (for H3). Therefore, an HVR includes residues in positions described previously:

A) 24-34 (L1), 50-52 (L2), 91-96 (L3), 26-32 (H1), 53-55 (H2), and 96-101 (H3) (Chothia and Lesk, *J. Mol. Biol.* 196:901-917 (1987);

B) 24-34 of L1, 50-56 of L2, 89-97 of L3, 31-35B of H1, 50-65 of H2, and 95-102 of H3 (Kabat et al., *Sequences of Proteins of Immunological Interest*, 5th Ed. Public Health Service, National Institutes of Health, Bethesda, MD (1991).

C) 30-36 (L1), 46-55 (L2), 89-96 (L3), 30-35 (H1), 47-58 (H2), 93-100a-j (H3) (MacCallum et al. *J. Mol. Biol.* 262:732-745 (1996).

[0077] Hypervariable regions may comprise "extended hypervariable regions" as follows: 24-36 or 24-34 (L1), 46-56 or 50-56 (L2) and 89-97 (L3) in the VL and 26-35B (H1), 50-65, 47-65 or 49-65 (H2) and 93-102, 94-102 or 95-102 (H3)

in the VH. The variable domain residues are numbered according to Kabat *et al.*, *supra* for each of these definitions.

4. BRIEF DESCRIPTION OF FIGURES

[0078]

Figure 1 depicts the assay schematic for the factor D TR-FRET (Time Resolved-FRET) assay.

Figure 2 depicts the co-titration of Streptavidin-Alexa-Fluor 647 and anti-Factor Ba-Europium. Varying concentrations of the Streptavidin-Alexa-Fluor 647 and anti-Factor Ba-Europium were analyzed with fixed concentrations of the other reagents and then the assay was performed as described in Section 6.1, in order to optimize the signal of the TR-FRET assay.

Figure 3 depicts the TR-FRET ratios with different incubation times of the enzymatic reaction of the lampalizumab/Factor D/Factor B/Factor C3b mixture. Note that the activity of Factor D was greatly diminished when the detection reagents were added prior to initiation of the enzymatic reaction ($t=0$) and increased with increasing time.

Figure 4 depicts the TR-FRET ratios with different incubation times of the detection reagents (*i.e.*, the mixture of anti-Factor Bb, anti-Factor Ba-Europium and Streptavidin-Alexa Fluor 647).

Figures 5A and **5B** show that both the TR-FRET and the AlphaScreen detection technologies generated good signal and dynamic range.

5. DETAILED DESCRIPTION

[0079] The present invention provides methods of measuring Factor D activity comprising performing a proximity-based measurement assay, methods of determining the potency of Factor D inhibitors comprising performing a proximity-based measurement assay, and methods of screening for Factor D inhibitors comprising measuring Factor B cleaving using a proximity-based measurement assay. The methods are simple, fast, homogeneous and adaptable to high-throughput assays, and are based in part on the inventors' development and characterization of an assay that measures the ability of Factor D inhibitors (including lampalizumab (an anti-Factor D antibody)) to inhibit the enzymatic activity of Factor D (see Section 6). To more precisely measure Factor D activity or the potency of Factor D inhibitors, a quencher can be added to terminate the enzymatic cleavage of Factor B by Factor D before measuring. Luckily, the inventors have discovered that when both anti-Factor Ba and anti-Factor Bb are used as detection reagents, they quench the Factor D activity in the assay, therefore obviating the need to add another quencher.

5.1. Proximity-Based Measurement Assays

[0080] The proximity-based measurement assay performed according to the methods described herein can utilize any proximity-based technology known in the art for measuring the binding of a protein pair. Such assays utilize a proximity signal that is generated by an acceptor and/or a donor when the acceptor and the donor (each of which is part of, binds to, or is attached to one member of the protein pair) are brought to close proximity. Thus, the value of the proximity signal is sensitive to the distance between the acceptor and the donor. In some embodiments, the proximity signal is a signal generated by the acceptor and the donor which indicates that the acceptor and the donor (and thus the protein pair) are in proximity. In some embodiments, the proximity signal is a signal generated by the acceptor which indicates that the acceptor and the donor (and thus the protein pair) are in proximity. In some embodiments, the proximity signal is a signal generated by the donor which indicates that the acceptor and the donor (and thus the protein pair) are in proximity.

[0081] The donor/acceptor pair thus can be any pair of molecules that can generate a proximity signal whose value is sensitive to their distance. The donor and/or the acceptor may be attached to the molecule(s) of interest (*i.e.*, member(s) of the protein pair) by a protein (*e.g.*, an antibody or antigen-binding fragment thereof), peptide, peptide mimetic, aptamer, nucleotide (*e.g.*, DNA, RNA, shRNA, miRNA, siRNA, antisense DNA), or any other molecule that binds to the member of the protein pair, or by direct chemical labeling. The degree of proximity between the donor and the acceptor that is required to elicit a proximity signal is dependent on the specific technology employed. Non-limiting exemplary proximity-based technologies for measuring the binding of a protein pair include Fluorescence Resonance Energy Transfer (FRET) and other FRET-based methods such as Time Resolved-FRET (TR-FRET), AlphaScreen®, AlphaLISA®, and PCR-based proximity ligation assays (see for example, Morrison, 1988, *Anal Biochem* 174:101-120; Ullman et al., 1994, *Proc Natl Acad Sci U S A* 91: 5426-5430; Ullman et al., 1996, *Clin Chem* 42:1518-1526; Glickman et al., 2002, *Journal of Biomolecular Screening* 7:3-10; Bielefeld-Sevigny, 2009, *Assay Drug Dev Technol* 7:90-92; and Gullberg et al., 2004, *Proc Natl Acad Sci U S A* 101: 8420-8424).

[0082] Fluorescence resonance energy transfer (FRET) is the transfer of energy between a light-sensitive donor and a light-sensitive acceptor. The donor, after being excited by a light source, may transfer energy to the acceptor. The

transfer of energy leads to a reduction in the donor's fluorescence emission intensity and an increase in the acceptor's fluorescence emission intensity. The efficiency of this energy transfer is inversely proportional to the sixth power of the distance between donor and acceptor, making FRET extremely sensitive to small changes in distance, and making FRET useful in determining if the donor and the acceptor are within a certain distance of each other. When the proximity-based technology is Fluorescence Resonance Energy Transfer (FRET), the proximity signal can be the ratio between the FRET acceptor's fluorescence emission intensity and the FRET donor's fluorescence emission intensity that is higher than a baseline level (e.g., about 2-fold, 5-fold, 10-fold, 20-fold, 50-fold, 100-fold higher or more). A baseline level here is the ratio between the FRET acceptor's fluorescence emission intensity and the FRET donor's fluorescence emission intensity when the FRET acceptor and the FRET donor are apart (e.g., more than 10 nm, 20 nm, 50 nm, 100 nm, or 200 nm apart).

[0083] TR-FRET is a FRET technology that has introduced a time delay between the excitation of the donor and the fluorescence measurement to reduce or clear the non-specific interfering short-lived emission signals from the background (for example, buffers and cell lysates). The emission signals from the donor and the acceptor, however, are long-lived and will not be affected.

[0084] A pair of light-sensitive donor and acceptor molecules that interact in such a manner that FRET occurs is often referred to as a FRET pair, and is known to those skilled in the art. The mechanism of FRET-pair interaction requires that the excitation spectrum of the acceptor overlaps the emission spectrum of the donor (see, Stryer, 1978, *Ann Rev Biochem* 47:819-846; Cantor and Schimmel, 1980, *Biophysical Chemistry Part II: Techniques for the Study of Biological Structure And Function*, pages 448-455, San Francisco, CA: W. H. Freeman and Co.; and Selvin, 1995, *Methods in Enzymology* 246:300-335). The efficiency of FRET interaction is linearly proportional to this overlap (Haugland et al., 1969, *Proc Natl Acad Sci USA* 63:24-30). FRET pairs have been chosen on this basis.

[0085] Any of a number of FRET-pair combinations can be selected for use in the present invention (see for example, Pesce et al., eds, 1971, *Fluorescence Spectroscopy*, New York, NY: Marcel Dekker; White et al., 1970, *Fluorescence Analysis: A practical Approach*, New York, NY: Marcel Dekker; and Haugland, 1996, *Handbook of Fluorescent Probes and Research Chemicals*, 6th Ed, Eugene, OR: Molecular Probes, Inc.). In general, a preferred donor is selected that has an emission spectrum that substantially overlaps the acceptor's excitation spectrum. In such applications the use of intense laser light, high-powered LED, or xenon flash lamp can serve as an effective means to excite the donor. The acceptor has a substantial overlap of its excitation spectrum with the emission spectrum of the donor. In addition, the wavelength maximum of the emission spectrum of the acceptor is preferably at least 10 nm greater than the wavelength maximum of the excitation spectrum of the donor. The emission spectrum of the acceptor is typically in the red portion of the visible spectrum, although, it is believed that acceptors having emission at longer wavelengths in the infrared region of the spectrum can be used. In some embodiments, the donor comprises Europium, the acceptor comprises Alexa 647, and the light source has a wavelength of about 340 nm.

[0086] In order to obtain FRET between the donor and the acceptor, the two have to be in spatial proximity with each other. Thus, in certain embodiments, the assay components are labeled such that the donor and the acceptor can be about 0.1 nm, 0.5 nm, 1 nm, 5 nm, or 10 nm apart from each other, or less than about 10 nm to allow FRET to occur.

[0087] AlphaScreen® and AlphaLISA® are bead-based technologies, and the assays are conducted in a microplate format. The donor and the acceptor are in the form of beads. Donor beads contain a photosensitizer, phthalocyanine, which converts ambient oxygen to an excited and reactive form of O₂, singlet oxygen, upon illumination at 680 nm. Singlet oxygen has a limited lifetime prior to falling back to ground state. Within its 4 μsec half-life, singlet oxygen can diffuse approximately 200 nm in solution. If an acceptor bead is within that proximity, energy is transferred from the singlet oxygen to thioxene derivatives within the acceptor bead, subsequently culminating in light production at 520--620 nm (AlphaScreen) or at 615 nm (AlphaLISA). In the absence of an acceptor bead, singlet oxygen falls to ground state and no signal is produced. When the proximity-based technology is AlphaScreen®, the proximity signal can be the acceptor's emission intensity that is higher than a baseline level (e.g., about 2-fold, 5-fold, 10-fold, 20-fold, 50-fold, 100-fold higher or more). A baseline level here is the acceptor's emission intensity when the acceptor and the donor are apart (e.g., more than 200 nm, 300 nm, 400 nm, 500 nm, 1000 nm, 2000 nm apart).

[0088] In order to obtain proximity signal from the acceptor using the AlphaScreen® or the AlphaLISA® technology, the donor and the acceptor have to be in spatial proximity with each other. Thus, in certain embodiments, the assay components are labeled such that the donor and the acceptor can be about 1 nm, 5 nm, 10 nm, 25 nm, 50 nm, 75 nm, 100 nm, 125 nm, 150 nm, 175 nm, 200 nm apart from each other, or less than about 200 nm apart from each other to allow the proximity-dependent chemical energy transfer to occur.

[0089] In PCR-based proximity ligation assays, the donor and the acceptor each contains an oligonucleotide that can be ligated. The binding of the donor and the acceptor brings in close proximity the two oligonucleotides, which are then ligated, amplified, and detected by PCR.

[0090] In certain embodiments, the proximity-based measurement assay is carried out in a microplate. In specific embodiments, the proximity-based measurement assay is conducted in a high-throughput manner. In some embodiments, the donor and/or the acceptor is in the form of beads (e.g., AlphaScreen beads). In certain embodiments, the

donor and/or the acceptor comprises streptavidin, avidin, or neutravidin (preferably streptavidin) that can bind to biotin conjugated to an assay component. In certain embodiments, the donor and/or the acceptor is directly conjugated to an assay component.

5.2. The Assay Components

[0091] The substrate for Factor D is another alternative complement pathway serine protease, Factor B. Factor C3b binds to Factor B; then, Factor D cleaves Factor B into Factor Ba and Factor Bb. Factor Bb remains bound to Factor C3b, forming the active C3 convertase, which initiates the alternative complement pathway (Volanakis, et al., 1996, Protein Science 5:553-564). Therefore, if Factor B is not cleaved by Factor D, Factor Ba and Factor Bb will be in spatial proximity with each other, Factor C3b and Factor Ba will also be in spatial proximity with each other. When Factor B is cleaved by Factor D, however, Factor Ba and Factor Bb will be apart from each other, and Factor C3b and Factor Ba will also be apart from each other.

[0092] In certain embodiments, the methods described herein rely on the distance between Factor Ba and Factor Bb, wherein one of the two is labeled with a donor, and the other is labeled with an acceptor. In such embodiments, the donor and/or the acceptor may be attached to Factor Ba or Factor Bb, respectively, by a protein (e.g., an antibody or antigen-binding fragment thereof), peptide, peptide mimetic, aptamer, nucleotide (e.g., DNA, RNA, shRNA, miRNA, siRNA, antisense DNA), or any other molecule that binds to Factor Ba or Factor Bb, or by direct chemical labeling (when the donor is attached to Factor Ba, the acceptor is attached to Factor Bb; when the donor is attached to Factor Bb, the acceptor is attached to Factor Ba).

[0093] In certain embodiments, the methods described herein rely on the distance between Factor C3b and Factor Ba, wherein one of the two is labeled with a donor, and the other is labeled with an acceptor. In such embodiments, the donor and/or the acceptor may be attached to Factor C3b or Factor Ba, respectively, by a protein (e.g., an antibody or antigen-binding fragment thereof), peptide, peptide mimetic, aptamer, nucleotide (e.g., DNA, RNA, shRNA, miRNA, siRNA, antisense DNA), or any other molecule that binds to Factor C3b or Factor Ba, or by direct chemical labeling (when the donor is attached to Factor C3b, the acceptor is attached to Factor Ba; when the donor is attached to Factor Ba, the acceptor is attached to Factor C3b).

5.3. Methods of Measuring Factor D Activity

[0094] In one aspect, provided herein are method of measuring the activity of Factor D in a sample derived from a subject, comprising performing a proximity-based measurement assay, wherein the proximity-based measurement assay measures the cleavage of Factor B. The proximity-based measurement assay can utilize any proximity-base technology known in the art for measuring the binding of a protein pair, as described in Section 5.1. The methods described in this section are useful, for example, in diagnosing or staging a human patient having or suspected of having a disorder associated with increased or decreased Factor D activity relative to a normal person.

[0095] In various embodiments, the methods of measuring the activity of Factor D comprise (a) adding to the sample an anti-Factor Ba antibody labeled with a first moiety and an anti-Factor Bb antibody labeled with a second moiety, wherein one of the moieties is a donor, and the other moiety is an acceptor, and wherein a proximity signal generated by the acceptor and/or the donor indicates that Factor Ba and Factor Bb are in proximity; and (b) measuring the value of the proximity signal from the sample; wherein the activity of Factor D in the sample is negatively correlated with the value of the proximity signal.

[0096] In certain aspects of such various embodiments, the methods of measuring the activity of Factor D further comprise: (c) adding to a control sample the anti-Factor Ba antibody labeled with the first moiety and the anti-Factor Bb antibody labeled with the second moiety; and (d) measuring the value of the proximity signal from the control sample; wherein a greater value of the proximity signal from the sample relative to the control sample (e.g., about 10%, 15%, 20%, 25%, 30%, 40%, 50%, 60%, 70%, 80%, 90% greater or more, or about 1-fold, 1.5-fold, 2-fold, 3-fold, 4-fold, 5-fold, 6-fold, 7-fold, 8-fold, 9-fold, 10-fold, 15-fold, 20-fold, 30-fold, 40-fold, 50-fold greater or more) indicates a lower activity of Factor D in the sample relative to the control sample.

[0097] When the proximity signal generated by the donor and/or the acceptor is based on energy transfer between the donor and the acceptor upon light activation, in various embodiments, the methods of measuring the activity of Factor D comprise: (A) adding to the sample an anti-Factor Ba antibody labeled with a first moiety and an anti-Factor Bb antibody labeled with a second moiety, wherein one of the moieties is a donor, and the other moiety is an acceptor; (B) providing a light source to excite the donor in the sample; and (C) measuring the donor fluorescence emission intensity from the sample, and/or the acceptor fluorescence emission intensity from the sample; wherein the activity of Factor D in the sample is positively correlated with the donor fluorescence emission intensity from the sample, and/or is negatively correlated with the acceptor fluorescence emission intensity from the sample. In certain embodiments, the step of (C) is performed after a period of time of the step of (B) that results in a decrease in interfering short-lived background

signals. In specific embodiments, the methods of measuring the activity of Factor D further comprise: (D) adding to a control sample the anti-Factor Ba antibody labeled with the first moiety and the anti-Factor Bb antibody labeled with the second moiety; (E) providing the same light source to excite the donor in the control sample; and (F) measuring the donor fluorescence emission intensity from the control sample, and/or the acceptor fluorescence emission intensity from the control sample; wherein a lower donor fluorescence emission intensity from the sample relative to the control sample, and/or a higher acceptor fluorescence emission intensity from the sample relative to the control sample, indicates a lower activity of Factor D in the sample relative to the control sample. In certain embodiments, the step of (C) is performed after a period of time of the step of (B) that results in a decrease in interfering short-lived background signals, and the step of (F) is performed after the same period of time of the step of (E).

[0098] In certain embodiments, the anti-Factor Ba antibody and the anti-Factor Bb antibody used in the methods of measuring the activity of Factor D quench the activity of Factor D. In such embodiments, the need to add another quencher is obviated. In certain embodiments, the methods of measuring the activity of Factor D further comprise a step of quenching the activity of Factor D in the sample by providing an excessive amount of a quencher to the sample before the step of (a). When a control sample is used, in certain embodiments, the methods of measuring the activity of Factor D further comprise a step of quenching the activity of Factor D in the sample by providing an excessive amount of a quencher to the sample before the step of (a), and a step of quenching the activity of Factor D in the control sample by providing an excessive amount of the quencher to the control sample before the step of (c). In specific embodiments, the quencher is a Factor D inhibitor (for example, an anti-Factor D antibody or an excess amount of EDTA).

[0099] In certain embodiments, the anti-Factor Ba antibody is biotinylated, and the first moiety comprises streptavidin, avidin, or neutravidin. In some embodiments, the anti-Factor Ba antibody is biotinylated, and the first moiety comprises streptavidin. In certain embodiments, the anti-Factor Bb antibody is biotinylated, and the second moiety comprises streptavidin, avidin, or neutravidin. In some embodiments, the anti-Factor Bb antibody is biotinylated, and the second moiety comprises streptavidin.

[0100] In other various embodiments, the methods of measuring the activity of Factor D comprise (a) adding to the sample an anti-Factor C3b antibody labeled with a first moiety and an anti-Factor Ba antibody labeled with a second moiety, wherein one of the moieties is a donor, and the other moiety is an acceptor, and wherein a proximity signal generated by the acceptor and/or the donor indicates that Factor C3b and Factor Ba are in proximity; and (b) measuring the value of the proximity signal from the sample; wherein the activity of Factor D in the sample is negatively correlated with the value of the proximity signal.

[0101] In certain aspects of such other various embodiments, the methods of measuring the activity of Factor D further comprise: (c) adding to a control sample the anti-Factor C3b antibody labeled with the first moiety and the anti-Factor Ba antibody labeled with the second moiety; and (d) measuring the value of the proximity signal from the control sample; wherein a greater value of the proximity signal from the sample relative to the control sample (e.g., about 10%, 15%, 20%, 25%, 30%, 40%, 50%, 60%, 70%, 80%, 90% greater or more, or about 1-fold, 1.5-fold, 2-fold, 3-fold, 4-fold, 5-fold, 6-fold, 7-fold, 8-fold, 9-fold, 10-fold, 15-fold, 20-fold, 30-fold, 40-fold, 50-fold greater or more) indicates a lower activity of Factor D in the sample relative to the control sample.

[0102] When the proximity signal generated by the donor and/or the acceptor is based on energy transfer between the donor and the acceptor upon light activation, in various embodiments, the methods of measuring the activity of Factor D comprise: (A) adding to the sample an anti-Factor C3b antibody labeled with a first moiety and an anti-Factor Ba antibody labeled with a second moiety, wherein one of the moieties is a donor, and the other moiety is an acceptor; (B) providing a light source to excite the donor in the sample; and (C) measuring the donor fluorescence emission intensity from the sample, and/or the acceptor fluorescence emission intensity from the sample; wherein the activity of Factor D in the sample is positively correlated with the donor fluorescence emission intensity from the sample, and/or is negatively correlated with the acceptor fluorescence emission intensity from the sample. In certain embodiments, the step of (C) is performed after a period of time of the step of (B) that results in a decrease in interfering short-lived background signals. In specific embodiments, the methods of measuring the activity of Factor D further comprise: (D) adding to a control sample the anti-Factor C3b antibody labeled with the first moiety and the anti-Factor Ba antibody labeled with the second moiety; (E) providing the same light source to excite the donor in the control sample; and (F) measuring the donor fluorescence emission intensity from the control sample, and/or the acceptor fluorescence emission intensity from the control sample; wherein a lower donor fluorescence emission intensity from the sample relative to the control sample, and/or a higher FRET acceptor fluorescence emission intensity from the sample relative to the control sample, indicates a lower activity of Factor D in the sample relative to the control sample. In certain embodiments, the step of (C) is performed after a period of time of the step of (B) that results in a decrease in interfering short-lived background signals, and the step of (F) is performed after the same period of time of the step of (E).

[0103] In certain embodiments wherein anti-Factor C3b antibody and anti-Factor Ba antibody are used, the anti-Factor C3b antibody is biotinylated, and the first moiety comprises streptavidin, avidin, or neutravidin. In some embodiments, the anti-Factor C3b antibody is biotinylated, and the first moiety comprises streptavidin. In certain embodiments, the anti-Factor Ba antibody is biotinylated, and the second moiety comprises streptavidin, avidin, or neutravidin. In some

embodiments, the anti-Factor Ba antibody is biotinylated, and the second moiety comprises streptavidin.

[0104] In certain embodiments wherein anti-Factor C3b antibody and anti-Factor Ba antibody are used, the anti-Factor C3b antibody and the anti-Factor Ba antibody used in the methods of measuring the activity of Factor D quench the activity of Factor D. In such embodiments, the need to add another quencher is obviated. In certain embodiments wherein anti-Factor C3b antibody and anti-Factor Ba antibody are used, the methods of measuring the activity of Factor D further comprise a step of quenching the activity of Factor D in the sample by providing an excessive amount of a quencher to the sample before the step of (a). When a control sample is used, in certain embodiments, the methods of measuring the activity of Factor D further comprise a step of quenching the activity of Factor D in the sample by providing an excessive amount of a quencher to the sample before the step of (a), and a step of quenching the activity of Factor D in the control sample by providing an excessive amount of the quencher to the control sample before the step of (c). In specific embodiments, the quencher is a Factor D inhibitor (for example, an anti-Factor D antibody or an excess amount of EDTA).

[0105] The sample can comprise a tissue, a population of cells directed isolated from the subject, a population of cultured cells derived from the subject, or a preparation from the tissue, the population of cells or the population of cultured cells that allows the activity of Factor D to be measured. When a control sample is used, the control sample is preferably in the same format as the sample. The control sample can be, but is not limited to, a sample with known Factor D activity or a sample with no Factor D activity. In specific embodiments, more than one control sample is used in the methods described herein. In certain embodiments, a standard curve has been generated for quantifying the activity of Factor D in samples without the need to measure a control sample.

[0106] The donor/acceptor pair can be any known in the art, or as described in Section 5.1.

[0107] The subject referred to in the methods described herein, can be, but is not limited to, a human or non-human vertebrate such as a wild, domestic or farm animal. In certain embodiments, the subject is a mammal, e.g., a human, a cow, a dog, a cat, a goat, a horse, a sheep, a pig, a rat, or a mouse. In a preferred embodiment, the subject is a human. In some embodiments, the subject is a human patient having or suspected of having a disorder associated with increased or decreased Factor D activity relative to a normal person, such as age-related macular degeneration (AMD). In some embodiments, the subject is a human patient having or suspected of having a disorder associated with excessive or uncontrolled complement activation. They include: complement activation during cardiopulmonary bypass operations; complement activation due to ischemia-reperfusion following acute myocardial infarction, aneurysm, stroke, hemorrhagic shock, crush injury, multiple organ failure, hypobolemic shock and intestinal ischemia. These disorders associated with excessive or uncontrolled complement activation can also include disease or condition is an inflammatory condition such as severe burns, endotoxemia, septic shock, adult respiratory distress syndrome, hemodialysis; anaphylactic shock, severe asthma, angioedema, Crohn's disease, sickle cell anemia, poststreptococcal glomerulonephritis and pancreatitis. The disorder may be the result of an adverse drug reaction, drug allergy, IL-2 induced vascular leakage syndrome or radiographic contrast media allergy. It also includes autoimmune disease such as systemic lupus erythematosus, myasthenia gravis, rheumatoid arthritis, Alzheimer's disease and multiple sclerosis. Complement activation is also associated with transplant rejection. Complement activation is also associated with ocular diseases (all ocular conditions and diseases the pathology of which involve complement, including the classical and the alternative pathway of complement), such as, for example, without limitation, macular degenerative disease, such as all stages of age-related macular degeneration (AMD), including dry and wet (non-exudative and exudative) forms, diabetic retinopathy and other ischemia-related retinopathies, choroidal neovascularization (CNV), uveitis, diabetic macular edema, pathological myopia, von Hippel-Lindau disease, histoplasmosis of the eye, Central Retinal Vein Occlusion (CRVO), corneal neovascularization, and retinal neovascularization. In one example, complement-associated eye conditions include age-related macular degeneration (AMD), including non-exudative (e.g. intermediate dry AMD or geographic atrophy (GA)) and exudative (e.g. wet AMD (choroidal neovascularization (CNV)) AMD, diabetic retinopathy (DR), endophthalmitis and uveitis. In a further example, nonexudative AMD may include the presence of hard drusen, soft drusen, geographic atrophy and/or pigment clumping. In another example, complement-associated eye conditions include age-related macular degeneration (AMD), including early AMD (e.g. includes multiple small to one or more non-extensive medium sized drusen), intermediate AMD (e.g. includes extensive medium drusen to one or more large drusen) and advanced AMD (e.g. includes geographic atrophy or advanced wet AMD (CNV). In a further example, intermediate dry AMD may include large confluent drusen. In a further example, geographic atrophy may include photoreceptor and/or Retinal Pigmented Epithelial (RPE) loss. In a further example, the area of geographic atrophy may be small or large and/or may be in the macula area or in the peripheral retina. In one example, the complement-associated eye condition is intermediate dry AMD. In one example, the complement-associated eye condition is geographic atrophy. In one example, the complement-associated eye condition is wet AMD (choroidal neovascularization (CNV)).

[0108] In the methods of measuring the activity of Factor B described above, the anti-Factor Ba, anti-Factor Bb, and/or anti-Factor C3b may be replaced by a peptide, a non-antibody protein, a peptide mimetic, an aptamer, a nucleotide (e.g., DNA, RNA, shRNA, miRNA, siRNA, antisense DNA), or any other molecule that binds to Factor Ba, Factor Bb, or anti-Factor C3b, respectively. Alternatively, the Factor Ba, Factor Bb, and/or Factor C3b may be directed attached to

the donor or acceptor (as the case may be) by direct chemical labeling.

[0109] In specific embodiments of the methods of measuring the activity of Factor D described herein, the Factor B is a recombinantly expressed Factor B. In specific embodiments of the methods of measuring the activity of Factor D described herein, the Factor B is endogenously expressed Factor B purified from a sample derived from a subject.

[0110] The Factor D can be recombinantly expressed or endogenously expressed. In some embodiments, the Factor D is purified from the sample before the measuring of its activity.

[0111] The term "sample" referred to in the methods described herein, can be, but is not limited to, a blood sample or a serum sample.

5.4. Methods of Determining the Potency of Factor D Inhibitor

[0112] In another aspect, provided herein are methods of determining the potency of a Factor D inhibitor in inhibiting Factor D activity, comprising performing a proximity-based measurement assay, wherein the proximity-based measurement assay measures the cleavage of Factor B. The proximity-based measurement assay can utilize any proximity-based technology known in the art for measuring the binding of a protein pair, as described in Section 5.1. The methods described in this section are useful, for example, in assessing the quality of anti-Factor D therapeutics for quality control in batch manufacturing, and in testing the potency of selected anti-Factor D therapeutic leads.

[0113] In various embodiments, the methods of determining the potency of a Factor D inhibitor comprise: (a) mixing a Factor D inhibitor candidate with Factor D, Factor B and Factor C3b in a test reaction mix; (b) incubating the test reaction mix; (c) adding to the test reaction mix an anti-Factor Ba antibody labeled with a first moiety and an anti-Factor Bb antibody labeled with a second moiety after the step of (b), wherein one of the moieties is a donor, and the other is an acceptor, and wherein a proximity signal generated by the acceptor and/or the donor indicates that Factor Ba and Factor Bb are in proximity; and (d) measuring the value of the proximity signal from the test reaction mix; wherein the potency of the Factor D inhibitor is positively correlated with the value of the proximity signal.

[0114] In certain aspects of such various embodiments, the methods of determining the potency of a Factor D inhibitor further comprise: (e) mixing a control reaction mix; (f) incubating the control reaction mix; (g) adding to the control reaction mix the anti-Factor Ba antibody labeled with the first moiety and the anti-Factor Bb antibody labeled with the second moiety after the step of (f); and (h) measuring the value of the proximity signal from the control test reaction mix; wherein a greater value of the proximity signal from the test reaction mix relative to the control reaction mix (e.g., about 10%, 15%, 20%, 25%, 30%, 40%, 50%, 60%, 70%, 80%, 90% greater or more, or about 1-fold, 1.5-fold, 2-fold, 3-fold, 4-fold, 5-fold, 6-fold, 7-fold, 8-fold, 9-fold, 10-fold, 15-fold, 20-fold, 30-fold, 40-fold, 50-fold greater or more) indicates a greater inhibition of Factor D activity by the Factor D inhibitor in the test reaction mix relative to the control reaction mix.

[0115] When the proximity signal generated by the donor and/or the acceptor is based on energy transfer between the donor and the acceptor upon light activation, in various embodiments, the methods of determining the potency of a Factor D inhibitor comprise: (A) mixing the Factor D inhibitor with Factor D, Factor B and Factor C3b in a test reaction mix; (B) incubating the test reaction mix; (C) adding to the test reaction mix an anti-Factor Ba antibody labeled with a first moiety and an anti-Factor Bb antibody labeled with a second moiety after the step of (B), wherein one of the moieties is a donor, and the other moiety is an acceptor; (D) providing a light source to excite the donor in the test reaction mix; and (E) measuring the donor fluorescence emission intensity from the test reaction mix, and/or the acceptor fluorescence emission intensity from the test reaction mix; wherein the potency of the Factor D inhibitor is negatively correlated with the donor fluorescence emission intensity from the test reaction mix, and/or is positively correlated with the acceptor fluorescence emission intensity from the test reaction mix. In specific embodiments, the step of (B) is conducted for about 15 min, 30 min, 45 min, 60 min, 75 min, or 90 min. In some embodiments, the step of (B) is conducted for about 45 min. In certain embodiments, the step of (E) is performed after a period of time of the step of (D) that results in a decrease in interfering short-lived background signals. In specific embodiments, the methods of determining the potency of a Factor D inhibitor further comprise: (F) mixing a control reaction mix; (G) incubating the control reaction mix; (H) adding to the control reaction mix the anti-Factor Ba antibody labeled with the first moiety and the anti-Factor Bb antibody labeled with the second moiety after the step of (G); (I) providing the same light source to excite the donor in the control reaction mix; and (J) measuring the donor fluorescence emission intensity from the control reaction mix, and/or the acceptor fluorescence emission intensity from the control reaction mix; wherein a lower donor fluorescence emission intensity from the test reaction mix relative to the control reaction mix, and/or a higher acceptor fluorescence emission intensity from the test reaction mix relative to the control reaction mix, indicates a greater inhibition of Factor D activity by the Factor D inhibitor in the test reaction mix relative to the control reaction mix. In specific embodiments, the steps of (B) and (G) are conducted for about 15 min, 30 min, 45 min, 60 min, 75 min, or 90 min. In some embodiments, the steps of (B) and (G) are conducted for about 45 min. In certain embodiments, the step of (E) is performed after a period of time of the step of (D) that results in a decrease in interfering short-lived background signals, and the step of (J) is performed after the same period of time of the step of (I).

[0116] In certain embodiments, the anti-Factor Ba antibody and the anti-Factor Bb antibody used in the method of

determining the potency of a Factor D inhibitor quench the activity of Factor D. In such embodiments, the need to add another quencher specifically is obviated. In certain embodiments, the method of determining the potency of a Factor D inhibitor further comprise a step of quenching the activity of Factor D in the sample by providing an excessive amount of a quencher to the sample before the step of (c). When a control sample is used, in certain embodiments, the methods of measuring the activity of Factor D further comprise a step of quenching the activity of Factor D in the sample by providing an excessive amount of a quencher to the sample before the step of (c), and a step of quenching the activity of Factor D in the control sample by providing an excessive amount of the quencher to the control sample before the step of (g). In specific embodiments, the quencher is a Factor D inhibitor (for example, an anti-Factor D antibody or an excess amount of EDTA).

[0117] In certain embodiments, the anti-Factor Ba antibody is biotinylated, and the first moiety comprises streptavidin, avidin, or neutravidin. In some embodiments, the anti-Factor Ba antibody is biotinylated, and the first moiety comprises streptavidin. In certain embodiments, the anti-Factor Bb antibody is biotinylated, and the second moiety comprises streptavidin, avidin, or neutravidin. In some embodiments, the anti-Factor Bb antibody is biotinylated, and the second moiety comprises streptavidin.

[0118] In other various embodiments, the methods of determining the potency of a Factor D inhibitor comprise: (a) mixing a Factor D inhibitor candidate with Factor D, Factor B and Factor C3b in a test reaction mix; (b) incubating the test reaction mix; (c) adding to the test reaction mix an anti-Factor C3b antibody labeled with a first moiety and an anti-Factor Ba antibody labeled with a second moiety after the step of (b), wherein one of the moieties is a donor, and the other is an acceptor, and wherein a proximity signal generated by the acceptor and/or the donor indicates that Factor C3b and Factor Ba are in proximity; and (d) measuring the value of the proximity signal from the test reaction mix; wherein the potency of the Factor D inhibitor is positively correlated with the value of the proximity signal.

[0119] In certain aspects of such other various embodiments, the methods of determining the potency of a Factor D inhibitor further comprise: (e) mixing a control reaction mix; (f) incubating the control reaction mix; (g) adding to the control reaction mix the anti-Factor C3b antibody labeled with the first moiety and the anti-Factor Ba antibody labeled with the second moiety after the step of (f); and (h) measuring the value of the proximity signal from the control test reaction mix; wherein a greater value of the proximity signal from the test reaction mix relative to the control reaction mix (e.g., about 10%, 15%, 20%, 25%, 30%, 40%, 50%, 60%, 70%, 80%, 90% greater or more, or about 1-fold, 1.5-fold, 2-fold, 3-fold, 4-fold, 5-fold, 6-fold, 7-fold, 8-fold, 9-fold, 10-fold, 15-fold, 20-fold, 30-fold, 40-fold, 50-fold greater or more) indicates a greater inhibition of Factor D activity by the Factor D inhibitor in the test reaction mix relative to the control reaction mix.

[0120] When the proximity signal generated by the donor and/or the acceptor is based on energy transfer between the donor and the acceptor upon light activation, in various embodiments, the methods of determining the potency of a Factor D inhibitor comprise: (A) mixing the Factor D inhibitor with Factor D, Factor B and Factor C3b in a test reaction mix; (B) incubating the test reaction mix; (C) adding to the test reaction mix an anti-Factor C3b antibody labeled with a first moiety and an anti-Factor Ba antibody labeled with a second moiety after the step of (B), wherein one of the moieties is a donor, and the other moiety is an acceptor; (D) providing a light source to excite the donor in the test reaction mix; and (E) measuring the donor fluorescence emission intensity from the test reaction mix, and/or the acceptor fluorescence emission intensity from the test reaction mix; wherein the potency of the Factor D inhibitor is negatively correlated with the donor fluorescence emission intensity from the test reaction mix, and/or is positively correlated with the acceptor fluorescence emission intensity from the test reaction mix. In specific embodiments, the step of (B) is conducted for about 15 min, 30 min, 45 min, 60 min, 75 min, or 90 min. In some embodiments, the step of (B) is conducted for about 45 min. In certain embodiments, the step of (E) is performed after a period of time of the step of (D) that results in a decrease in interfering short-lived background signals. In specific embodiments, the methods of determining the potency of a Factor D inhibitor further comprise: (F) mixing a control reaction mix; (G) incubating the control reaction mix; (H) adding to the control reaction mix the anti-Factor C3b antibody labeled with the first moiety and the anti-Factor Ba antibody labeled with the second moiety after the step of (G); (I) providing said light source to excite the donor in the control reaction mix; and (J) measuring the donor fluorescence emission intensity from the control reaction mix, and/or the acceptor fluorescence emission intensity from the control reaction mix; wherein a lower donor fluorescence emission intensity from the test reaction mix relative to the control reaction mix, and/or a higher acceptor fluorescence emission intensity from the test reaction mix relative to the control reaction mix, indicates a greater inhibition of Factor D activity by the Factor D inhibitor in the test reaction mix relative to the control reaction mix. In specific embodiments, the steps of (B) and (G) are conducted for about 15 min, 30 min, 45 min, 60 min, 75 min, or 90 min. In some embodiments, the steps of (B) and (G) are conducted for about 45 min. In certain embodiments, the step of (E) is performed after a period of time of the step of (D) that results in a decrease in interfering short-lived background signals, and the step of (J) is performed after the same period of time of the step of (I).

[0121] In certain embodiments wherein anti-Factor C3b antibody and anti-Factor Ba antibody are used, the anti-Factor C3b antibody is biotinylated, and the first moiety comprises streptavidin, avidin, or neutravidin. In some embodiments, the anti-Factor C3b antibody is biotinylated, and the first moiety comprises streptavidin. In certain embodiments, the

anti-Factor Ba antibody is biotinylated, and the second moiety comprises streptavidin, avidin, or neutravidin. In some embodiments, the anti-Factor Ba antibody is biotinylated, and the second moiety comprises streptavidin.

[0122] In certain embodiments wherein anti-Factor C3b antibody and anti-Factor Ba antibody are used, the anti-Factor C3b antibody and the anti-Factor Ba antibody used in the method of determining the potency of a Factor D inhibitor quench the activity of Factor D. In such embodiments, the need to add another quencher specifically is obviated. In certain embodiments wherein anti-Factor C3b antibody and anti-Factor Ba antibody are used, the method of determining the potency of a Factor D inhibitor further comprise a step of quenching the activity of Factor D in the sample by providing an excessive amount of a quencher to the sample before the step of (c). When a control sample is used, in certain embodiments, the method of determining the potency of a Factor D inhibitor further comprise a step of quenching the activity of Factor D in the sample by providing an excessive amount of a quencher to the sample before the step of (c), and a step of quenching the activity of Factor D in the control sample by providing an excessive amount of the quencher to the control sample before the step of (g). In specific embodiments, the quencher is a Factor D inhibitor (for example, an anti-Factor D antibody or an excess amount of EDTA).

[0123] The control reaction mix can comprise, for example, a different Factor D inhibitor with known potency (e.g., 100% potency) or no Factor D inhibitor, but contains everything else essentially the same as the test reaction mix. A quencher as described above can be used as a different Factor D inhibitor in the control reaction mix. In specific embodiments, more than one control reaction mix is used in the methods described herein. In certain embodiments, a standard curve has been generated for quantifying the potency of Factor D inhibitors in samples without the need to measure a control reaction mix.

[0124] The donor/acceptor pair can be any known in the art, or as described in Section 5.1.

[0125] The Factor D inhibitor can be any pharmaceutical agent that reduces or blocks the activity of Factor D.

[0126] In specific embodiments, the Factor D inhibitor is an antibody or an antigen-binding fragment thereof, for example, an antibody or an antigen-binding fragment thereof that binds to Factor D (see for example, International Patent Application Publication No. WO 1999/042133, International Patent Application Publication No. WO 2007/056227, International Patent Application Publication No. WO 2008/055206, International Patent Application Publication No. WO 2008/147883, and International Patent Application Publication No. WO 2009/134711, the disclosures of which are hereby incorporated by reference herein in their entireties). In some embodiments, the antibody is a murine antibody. In other embodiments, the antibody is a humanized antibody. In specific embodiments, the antibody is a bispecific antibody (e.g., a bispecific antibody that binds to Factor D and HTRA1). In some embodiments, the antibody is lampalizumab (see, International Patent Application Publication No. WO 2009/134711, the disclosure of which is hereby incorporated by reference herein in its entirety).

[0127] In some embodiments, the antibody comprises one, two, three, four, five or six of the following HVRs: (i) an HVR-H1 comprising the amino acid sequence of SEQ ID NO: 1; (ii) an HVR-H2 comprising the amino acid sequence of SEQ ID NO: 2, SEQ ID NO: 3, or SEQ ID NO: 4; (iii) an HVR-H3 comprising the amino acid sequence of SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, or SEQ ID NO: 8; (iv) an HVR-L1 comprising the amino acid sequence of SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, or SEQ ID NO: 17; (v) an HVR-L2 comprising the amino acid sequence of SEQ ID NO: 18; or (vi) an HVR-L3 comprising the amino acid sequence of SEQ ID NO: 19 or SEQ ID NO: 20 (see Table 1).

[0128] In some embodiments, the antibody comprises one, two, three, four, five or six of the following HVRs: (i) an HVR-H1 comprising the amino acid sequence of SEQ ID NO: 85; (ii) an HVR-H2 comprising the amino acid sequence of SEQ ID NO: 86, SEQ ID NO: 87, SEQ ID NO: 88, SEQ ID NO: 89, SEQ ID NO: 90, SEQ ID NO: 91, SEQ ID NO: 92, SEQ ID NO: 93, or SEQ ID NO: 94; (iii) an HVR-H3 comprising the amino acid sequence of SEQ ID NO: 95; (iv) an HVR-L1 comprising the amino acid sequence of SEQ ID NO: 96; (v) an HVR-L2 comprising the amino acid sequence of SEQ ID NO: 97, SEQ ID NO: 98, or SEQ ID NO: 99; or (vi) an HVR-L3 comprising the amino acid sequence of SEQ ID NO: 100 or SEQ ID NO: 101 (see Table 2).

Table 1. HVR amino acid sequences (in accordance with Kabat + Chothia HVR definitions) of anti-Factor D antibodies

Antibody	HVR-H1	HVR-H2	HVR-H3	HVR-L1	HVR-L2	HVR-L3
AFD WT	GYTFTNYGMN SEQ ID NO: 1	WINTYTGET TYADDFKG SEQ ID NO: 2	EGGVNN SEQ ID NO: 5	ITSTDIDDDMN SEQ ID NO: 9	GGNTLRP SEQ ID NO: 18	LQSDSLPYT SEQ ID NO: 19
AFD.v1	GYTFTNYGMN SEQ ID NO: 1	WINTYTGET TYADDFKG SEQ ID NO: 2	EGGVNN SEQ ID NO: 5	ITSTSIDDDMN SEQ ID NO: 10	GGNTLRP SEQ ID NO: 18	LQSDSLPYT SEQ ID NO: 19

EP 3 666 901 A1

(continued)

	Antibody	HVR-H1	HVR-H2	HVR-H3	HVR-L1	HVR-L2	HVR-L3
5	AFD.v2	GYTFTNYGMN SEQ ID NO: 1	WINTYTGET TYADDFKG SEQ ID NO: 2	EGGVNN SEQ ID NO: 5	ITSTDIEDDMN SEQ ID NO: 11	GGNTRLRP SEQ ID NO: 18	LQSDSLPYT SEQ ID NO: 19
10	AFD.v3	GYTFTNYGMN SEQ ID NO: 1	WINTYTGET TYADDFKG SEQ ID NO: 2	EGGVNN SEQ ID NO: 5	ITSTDIDSDMN SEQ ID NO: 12	GGNTRLRP SEQ ID NO: 18	LQSDSLPYT SEQ ID NO: 19
15	AFD.v4	GYTFTNYGMN SEQ ID NO: 1	WINTYTGET TYADDFKG SEQ ID NO: 2	EGGVNN SEQ ID NO: 5	ITSTDIDDSMN SEQ ID NO: 13	GGNTRLRP SEQ ID NO: 18	LQSDSLPYT SEQ ID NO: 19
	AFD.v5	GYTFTNYGMN SEQ ID NO: 1	WINTYTGET TYADDFKG SEQ ID NO: 2	EGGVNN SEQ ID NO: 5	ITSTSIDSSMN SEQ ID NO: 14	GGNTRLRP SEQ ID NO: 18	LQSDSLPYT SEQ ID NO: 19
20	AFD.v6	GYTFTNYGMN SEQ ID NO: 1	WINTYTGET TYAEDFKG SEQ ID NO: 3	EGGVNN SEQ ID NO: 5	ITSTDIESDMN SEQ ID NO: 15	GGNTRLRP SEQ ID NO: 18	LQSDSLPYT SEQ ID NO: 19
25	AFD.v7	GYTFTNYGMN 1 SEQ ID NO:	WINTYTGET TYAEDFKG SEQ ID NO: 3	EGGVNN SEQ ID NO: 5	ITSTDIESDMN SEQ ID NO: 15	GGNTRLRP SEQ ID NO: 18	LQSESLPYT SEQ ID NO: 20
30	AFD.v8	GYTFTNYGMN SEQ ID NO: 1	WINTYTGET TYAEDFKG SEQ ID NO: 3	EGGVNN SEQ ID NO: 5	ITSTSIESDMN SEQ ID NO: 16	GGNTRLRP SEQ ID NO: 18	LQSDSLPYT SEQ ID NO: 19
	AFD.v9	GYTFTNYGMN SEQ ID NO: 1	WINTYTGET TYAEDFKG SEQ ID NO: 3	EGGVNN SEQ ID NO: 5	ITSTSIESDMS SEQ ID NO: 17	GGNTRLRP SEQ ID NO: 18	LQSDSLPYT SEQ ID NO: 19
35	AFD.v10	GYTFTNYGMN SEQ ID NO: 1	WINTYTGET TYAEDFKG SEQ ID NO: 3	EGGVNN SEQ ID NO: 5	ITSTSIESDMN SEQ ID NO: 16	GGNTRLRP SEQ ID NO: 18	LQSESLPYT SEQ ID NO: 20
40	AFD.v11	GYTFTNYGMN SEQ ID NO: 1	WISTYTGET TYAEDFKG SEQ ID NO: 4	EGGVNN SEQ ID NO: 5	ITSTSIESDMN SEQ ID NO: 16	GGNTRLRP SEQ ID NO: 18	LQSDSLPYT SEQ ID NO: 19
45	AFD.v12	GYTFTNYGMN SEQ ID NO: 1	WINTYTGET TYAEDFKG SEQ ID NO: 3	EGGVND SEQ ID NO: 6	ITSTSIESDMN SEQ ID NO: 16	GGNTRLRP SEQ ID NO: 18	LQSDSLPYT SEQ ID NO: 19
	AFD.v13	GYTFTNYGMN SEQ ID NO: 1	WINTYTGET TYAEDFKG SEQ ID NO: 3	EGGVQN SEQ ID NO: 7	ITSTSIESDMN SEQ ID NO: 16	GGNTRLRP SEQ ID NO: 18	LQSDSLPYT SEQ ID NO: 19
50	AFD.v14	GYTFTNYGMN SEQ ID NO: 1	WINTYTGET TYAEDFKG SEQ ID NO: 3	EGGVSN SEQ ID NO: 8	ITSTSIESDMN SEQ ID NO: 16	GGNTRLRP SEQ ID NO: 18	LQSDSLPYT SEQ ID NO: 19
55	AFD.v15	GYTFTNYGMN SEQ ID NO: 1	WINTYTGET TYAEDFKG SEQ ID NO: 3	EGGVSN SEQ ID NO: 8	ITSTSIESDMN SEQ ID NO: 16	GGNTRLRP SEQ ID NO: 18	LQSESLPYT SEQ ID NO: 20

Table 2. HVR amino acid sequences (in accordance with Kabat HVR definitions) of additional anti-Factor D antibodies

Antibody	HVR-H1	HVR-H2	HVR-H3	HVR-L1	HVR-L2	HVR-L3
murine AFD	SYMY SEQ ID NO: 85	EINPTNGGTN FNEKFKS SEQ ID NO: 86	EGGFAY SEQ ID NO: 95	KASQNVDTDVA SEQ ID NO: 96	SASSRYS SEQ ID NO: 97	QQYNNYPLT SEQ ID NO: 100
huAFD.v2.0	SYMY SEQ ID NO: 85	EINPTSGGTN FNEKFKS SEQ ID NO: 87	EGGFAY SEQ ID NO: 95	KASQNVDTDVA SEQ ID NO: 96	SASSRYS SEQ ID NO: 97	QQYNNYPLT SEQ ID NO: 100
huAFD.v2.1	SYMY SEQ ID NO: 85	EINPTSGGTN FNEKFKS SEQ ID NO: 87	EGGFAY SEQ ID NO: 95	KASQNVDTDVA SEQ ID NO: 96	SASSRYS SEQ ID NO: 97	QQYNNYPLT SEQ ID NO: 100
huAFD.v2.3	SYMY SEQ ID NO: 85	EINPYSGDTN FNEKFKS SEQ ID NO: 88	EGGFAY SEQ ID NO: 95	KASQNVDTDVA SEQ ID NO: 96	SASSRYS SEQ ID NO: 97	QQYNNYPLT SEQ ID NO: 100
huAFD.v1	SYMY SEQ ID NO: 85	EINPTNGGTN FNEKFKS SEQ ID NO: 86	EGGFAY SEQ ID NO: 95	KASQNVDTDVA SEQ ID NO: 96	SASSRYS SEQ ID NO: 97	QQYNNYPLT SEQ ID NO: 100
huAFD.v1.1	SYMY SEQ ID NO: 85	EINPTQGGTN FNEKFKS SEQ ID NO: 89	EGGFAY SEQ ID NO: 95	KASQNVDTDVA SEQ ID NO: 96	SASSRYS SEQ ID NO: 97	QQYNNYPLT SEQ ID NO: 100
huAFD.v2.2	SYMY SEQ ID NO: 85	EINPTSGDTN FNEKFKS SEQ ID NO: 90	EGGFAY SEQ ID NO: 95	KASQNVDTDVA SEQ ID NO: 96	SASSRYS SEQ ID NO: 97	QQYNNYPLT SEQ ID NO: 100
huAFD.v2.4	SYMY SEQ ID NO: 85	EINPTSGETN FNEKFKS SEQ ID NO: 91	EGGFAY SEQ ID NO: 95	KASQNVDTDVA SEQ ID NO: 96	SASSRYS SEQ ID NO: 97	QQYNNYPLT SEQ ID NO: 100
huAFD.v2.5	SYMY SEQ ID NO: 85	EINPYSGGTN FNEKFKS SEQ ID NO: 92	EGGFAY SEQ ID NO: 95	KASQNVDTDVA SEQ ID NO: 96	SASSRYS SEQ ID NO: 97	QQYNNYPLT SEQ ID NO: 100
huAFD.v2.6	SYMY SEQ ID NO: 85	EINPTSGGTN FNEKFKS SEQ ID NO: 87	EGGFAY SEQ ID NO: 95	KASQNVDTDVA SEQ ID NO: 96	SASSRYS SEQ ID NO: 97	QQYNNYPLT SEQ ID NO: 100
huAFD.v2.7	SYMY SEQ ID NO: 85	EINPTSGGTN FNEKFKS SEQ ID NO: 87	EGGFAY SEQ ID NO: 95	KASQNVDTDVA SEQ ID NO: 96	SASSRYS SEQ ID NO: 97	QQYNNYPLT SEQ ID NO: 100

(continued)

Antibody	HVR-H1	HVR-H2	HVR-H3	HVR-L1	HVR-L2	HVR-L3
huAFD.v2.8	SYMY SEQ ID NO: 85	EINPTSGGTN FNEKFKS SEQ ID NO: 87	EGGFAY SEQ ID NO: 95	KASQNVDTDVA SEQ ID NO: 96	SASSRYS SEQ ID NO: 97	QQYNNYPLT SEQ ID NO: 100
huAFD.v2.9	SYMY SEQ ID NO: 85	WINPTSGGTN FNEKFKS SEQ ID NO: 93	EGGFAY SEQ ID NO: 95	KASQNVDTDVA SEQ ID NO: 96	SASSRYS SEQ ID NO: 97	QQYNNYPLT SEQ ID NO: 100
huAFD.v2.10	SYMY SEQ ID NO: 85	EINPTSGGTN FNEKFKS SEQ ID NO: 87	EGGFAY SEQ ID NO: 95	KASQNVDTDVA SEQ ID NO: 96	SASSRKS SEQ ID NO: 98	QQYNNYPLT SEQ ID NO: 100
huAFD.v2.11	SYMY SEQ ID NO: 85	EINPTSGGTN FNEKFKS SEQ ID NO: 87	EGGFAY SEQ ID NO: 95	KASQNVDTDVA SEQ ID NO: 96	SASSRRS SEQ ID NO: 99	QQYNNYPLT SEQ ID NO: 100
huAFD.v2.12	SYMY SEQ ID NO: 85	EINPYSGGTN FNEKFKS SEQ ID NO: 92	EGGFAY SEQ ID NO: 95	KASQNVDTDVA SEQ ID NO: 96	SASSRYS SEQ ID NO: 97	QQYNNYPLT SEQ ID NO: 100
huAFD.v2.13	SYMY SEQ ID NO: 85	EINPTSGGTN FNEKFKS SEQ ID NO: 87	EGGFAY SEQ ID NO: 95	KASQNVDTDVA SEQ ID NO: 96	SASSRYS SEQ ID NO: 97	QQYENYPLT SEQ ID NO: 101
huAFD.v2.14	SYMY SEQ ID NO: 85	EINPTSGETN FNEKFKS SEQ ID NO: 91	EGGFAY SEQ ID NO: 95	KASQNVDTDVA SEQ ID NO: 96	SASSRYS SEQ ID NO: 97	QQYNNYPLT SEQ ID NO: 100
huAFD.v2.15	SYMY SEQ ID NO: 85	EINPYSETN FNEKFKS SEQ ID NO: 94	EGGFAY SEQ ID NO: 95	KASQNVDTDVA SEQ ID NO: 96	SASSRYS SEQ ID NO: 97	QQYNNYPLT SEQ ID NO: 100

[0129] In some embodiments, the antibody comprises an HVR-H1 comprising the amino acid sequence of SEQ ID NO: 1, an HVR-H2 comprising the amino acid sequence of SEQ ID NO: 2, and an HVR-H3 comprising the amino acid sequence of SEQ ID NO: 5.

[0130] In some embodiments, the antibody comprises an HVR-H1 comprising the amino acid sequence of SEQ ID NO: 1, an HVR-H2 comprising the amino acid sequence of SEQ ID NO: 3, and an HVR-H3 comprising the amino acid sequence of SEQ ID NO: 5.

[0131] In some embodiments, the antibody comprises an HVR-H1 comprising the amino acid sequence of SEQ ID NO: 1, an HVR-H2 comprising the amino acid sequence of SEQ ID NO: 4, and an HVR-H3 comprising the amino acid sequence of SEQ ID NO: 5.

[0132] In some embodiments, the antibody comprises an HVR-H1 comprising the amino acid sequence of SEQ ID NO: 1, an HVR-H2 comprising the amino acid sequence of SEQ ID NO: 3, and an HVR-H3 comprising the amino acid sequence of SEQ ID NO: 6.

[0133] In some embodiments, the antibody comprises an HVR-H1 comprising the amino acid sequence of SEQ ID NO: 1, an HVR-H2 comprising the amino acid sequence of SEQ ID NO: 3, and an HVR-H3 comprising the amino acid sequence of SEQ ID NO: 7.

[0134] In some embodiments, the antibody comprises an HVR-H1 comprising the amino acid sequence of SEQ ID NO: 1, an HVR-H2 comprising the amino acid sequence of SEQ ID NO: 3, and an HVR-H3 comprising the amino acid sequence of SEQ ID NO: 8.

[0135] In some embodiments, the antibody comprises an HVR-L1 comprising the amino acid sequence of SEQ ID NO: 9, an HVR-L2 comprising the amino acid sequence of SEQ ID NO: 18, and an HVR-L3 comprising the amino acid sequence of SEQ ID NO: 19.

[0136] In some embodiments, the antibody comprises an HVR-L1 comprising the amino acid sequence of SEQ ID NO: 10, an HVR-L2 comprising the amino acid sequence of SEQ ID NO: 18, and an HVR-L3 comprising the amino acid

of SEQ ID NO: 52. In some embodiments, the antibody comprises a light chain variable domain having at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 52. See Table 3.

[0234] In some embodiments, the antibody comprises a heavy chain variable domain having the amino acid sequence of SEQ ID NO: 51, and a light chain variable domain having the amino acid sequence of SEQ ID NO: 52. In some embodiments, the antibody comprises a heavy chain variable domain having at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 51, and a light chain variable domain having at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 52. See Table 3.

Table 3. Heavy chain and light chain variable domain amino acid sequences of anti-Factor D antibodies

SEQ ID NO: 21	AFD WT Heavy Chain Variable Region	EVQLVQSGPELKKPGASVKVSCASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFSLDTSVSTAYLQISLKAEDTAVYYCEREGG VNNWGQGTLLTVSS
SEQ ID NO: 22	AFD WT Light Chain Variable Region	DIQVTQSPSSLSASVGDRVITITCITSTDIDDDMNWYQQKPGKVPKLLISGGNT LRPGVPSRFSGSGSGTDFTLTISLQPEDVATYYCLQSDSLPYTFGQGTKVEIK
SEQ ID NO: 23	AFD.v1 Heavy Chain Variable Region	EVQLVQSGPELKKPGASVKVSCASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFSLDTSVSTAYLQISLKAEDTAVYYCEREGG VNNWGQGTLLTVSS
SEQ ID NO: 24	AFD.v1 Light Chain Variable Region	DIQVTQSPSSLSASVGDRVITITCITSTSIDDDMNWYQQKPGKVPKLLISGGNT LRPGVPSRFSGSGSGTDFTLTISLQPEDVATYYCLQSDSLPYTFGQGTKVEIK
SEQ ID NO: 25	AFD.v2 Heavy Chain Variable Region	EVQLVQSGPELKKPGASVKVSCASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFSLDTSVSTAYLQISLKAEDTAVYYCEREGG VNNWGQGTLLTVSS
SEQ ID NO: 26	AFD.v2 Light Chain Variable Region	DIQVTQSPSSLSASVGDRVITITCITSTDIEDDMNWYQQKPGKVPKLLISGGNT LRPGVPSRFSGSGSGTDFTLTISLQPEDVATYYCLQSDSLPYTFGQGTKVEIK
SEQ ID NO: 27	AFD.v3 Heavy Chain Variable Region	EVQLVQSGPELKKPGASVKVSCASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFSLDTSVSTAYLQISLKAEDTAVYYCEREGG VNNWGQGTLLTVSS
SEQ ID NO: 28	AFD.v3 Light Chain Variable Region	DIQVTQSPSSLSASVGDRVITITCITSTDIDSDMNWYQQKPGKVPKLLISGGNT LRPGVPSRFSGSGSGTDFTLTISLQPEDVATYYCLQSDSLPYTFGQGTKVEIK
SEQ ID NO: 29	AFD.v4 Heavy Chain Variable Region	EVQLVQSGPELKKPGASVKVSCASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFSLDTSVSTAYLQISLKAEDTAVYYCEREGG VNNWGQGTLLTVSS

EP 3 666 901 A1

(continued)

5	SEQ ID NO: 30	AFD.v4 Light Chain Variable Region	DIQVTQSPSSLSASVGDRVITITCITSTDIDDSMNWYQQKPGKVPKLLISGGNT LRPGVPSRFSGSGSGTDFTLTISLQPEDVATYYCLQSDSLPYTFGQGTKVEIK
10	SEQ ID NO: 31	AFD.v5 Heavy Chain Variable Region	EVQLVQSGPELKKPGASVKVSCASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFSLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSS
15	SEQ ID NO: 32	AFD.v5 Light Chain Variable Region	DIQVTQSPSSLSASVGDRVITITCITSTSIDSMMNWYQQKPGKVPKLLISGGNTL RPGVPSRFSGSGSGTDFTLTISLQPEDVATYYCLQSDSLPYTFGQGTKVEIK
20	SEQ ID NO: 33	AFD.v6 Heavy Chain Variable Region	EVQLVQSGPELKKPGASVKVSCASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFSLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSS
25	SEQ ID NO: 34	AFD.v6 Light Chain Variable Region	DIQVTQSPSSLSASVGDRVITITCITSTDIESDMNWYQQKPGKVPKLLISGGNT LRPGVPSRFSGSGSGTDFTLTISLQPEDVATYYCLQSDSLPYTFGQGTKVEIK
30	SEQ ID NO: 35	AFD.v7 Heavy Chain Variable Region	EVQLVQSGPELKKPGASVKVSCASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFSLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSS
35	SEQ ID NO: 36	AFD.v7 Light Chain Variable Region	DIQVTQSPSSLSASVGDRVITITCITSTDIESDMNWYQQKPGKVPKLLISGGNT LRPGVPSRFSGSGSGTDFTLTISLQPEDVATYYCLQSDSLPYTFGQGTKVEIK
40	SEQ ID NO: 37	AFD.v8 Heavy Chain Variable Region	EVQLVQSGPELKKPGASVKVSCASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFSLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSS
45	SEQ ID NO: 38	AFD.v8 Light Chain Variable Region	DIQVTQSPSSLSASVGDRVITITCITSTSIESDMNWYQQKPGKVPKLLISGGNTL RPGVPSRFSGSGSGTDFTLTISLQPEDVATYYCLQSDSLPYTFGQGTKVEIK
50	SEQ ID NO: 39	AFD.v9 Heavy Chain Variable Region	EVQLVQSGPELKKPGASVKVSCASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFSLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSS
55	SEQ ID NO: 40	AFD.v9 Light Chain Variable Region	DIQVTQSPSSLSASVGDRVITITCITSTSIESDMSWYQQKPGKVPKLLISGGNTL RPGVPSRFSGSGSGTDFTLTISLQPEDVATYYCLQSDSLPYTFGQGTKVEIK

(continued)

5	SEQ ID NO: 41	AFD.v10 Heavy Chain Variable Region	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFSLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSS
10	SEQ ID NO: 42	AFD.v10 Light Chain Variable Region	DIQVTQSPSSLSASVGDRVTTTCITSTSIESDMNWDYQQKPGKVPKLLISGGNTL RPGVPSRFSGSGSGTDFTLTISSLQPEDVATYYCLQSESLPYTFGQGTKVEIK
15	SEQ ID NO: 43	AFD.v11 Heavy Chain Variable Region	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WISTYTGETTYAEDFKGRFVFSLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSS
20	SEQ ID NO: 44	AFD.v11 Light Chain Variable Region	DIQVTQSPSSLSASVGDRVTTTCITSTSIESDMNWDYQQKPGKVPKLLISGGNTL RPGVPSRFSGSGSGTDFTLTISSLQPEDVATYYCLQSDSLPYTFGQGTKVEIK
25	SEQ ID NO: 45	AFD.v12 Heavy Chain Variable Region	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFSLDTSVSTAYLQISSLKAEDTAVYYCEREGG VDNWGQGTLLTVSS
30	SEQ ID NO: 46	AFD.v12 Light Chain Variable Region	DIQVTQSPSSLSASVGDRVTTTCITSTSIESDMNWDYQQKPGKVPKLLISGGNTL RPGVPSRFSGSGSGTDFTLTISSLQPEDVATYYCLQSDSLPYTFGQGTKVEIK
35	SEQ ID NO: 47	AFD.v13 Heavy Chain Variable Region	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFSLDTSVSTAYLQISSLKAEDTAVYYCEREGG VQNWGQGTLLTVSS
40	SEQ ID NO: 48	AFD.v13 Light Chain Variable Region	DIQVTQSPSSLSASVGDRVTTTCITSTSIESDMNWDYQQKPGKVPKLLISGGNTL RPGVPSRFSGSGSGTDFTLTISSLQPEDVATYYCLQSDSLPYTFGQGTKVEIK
45	SEQ ID NO: 49	AFD.v14 Heavy Chain Variable Region	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFSLDTSVSTAYLQISSLKAEDTAVYYCEREGG VSNWGQGTLLTVSS
50	SEQ ID NO: 50	AFD.v14 Light Chain Variable Region	DIQVTQSPSSLSASVGDRVTTTCITSTSIESDMNWDYQQKPGKVPKLLISGGNTL RPGVPSRFSGSGSGTDFTLTISSLQPEDVATYYCLQSDSLPYTFGQGTKVEIK
55	SEQ ID NO: 51	AFD.v15 Heavy Chain Variable Region	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFSLDTSVSTAYLQISSLKAEDTAVYYCEREGG VSNWGQGTLLTVSS

5

10

15

20

25

30

35

40

45

50

55

[0248] In some embodiments, the antibody comprises a light chain variable domain having the amino acid sequence of SEQ ID NO: 111. In some embodiments, the antibody comprises a light chain variable domain having at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 111. See Table 4.

of SEQ ID NO: 132. In some embodiments, the antibody comprises a heavy chain variable domain having at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 132. See Table 4.

[0281] In some embodiments, the antibody comprises a light chain variable domain having the amino acid sequence of SEQ ID NO: 133. In some embodiments, the antibody comprises a light chain variable domain having at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 133. See Table 4.

[0282] In some embodiments, the antibody comprises a heavy chain variable domain having the amino acid sequence of SEQ ID NO: 132, and a light chain variable domain having the amino acid sequence of SEQ ID NO: 133. In some embodiments, the antibody comprises a heavy chain variable domain having at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 132, and a light chain variable domain having at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 133. See Table 4.

[0283] In some embodiments, the antibody comprises a heavy chain variable domain having the amino acid sequence of SEQ ID NO: 134. In some embodiments, the antibody comprises a heavy chain variable domain having at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 134. See Table 4.

[0284] In some embodiments, the antibody comprises a light chain variable domain having the amino acid sequence of SEQ ID NO: 135. In some embodiments, the antibody comprises a light chain variable domain having at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 135. See Table 4.

[0285] In some embodiments, the antibody comprises a heavy chain variable domain having the amino acid sequence of SEQ ID NO: 134, and a light chain variable domain having the amino acid sequence of SEQ ID NO: 135. In some embodiments, the antibody comprises a heavy chain variable domain having at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 134, and a light chain variable domain having at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 135. See Table 4.

[0286] In some embodiments, the antibody comprises a heavy chain variable domain having the amino acid sequence of SEQ ID NO: 136. In some embodiments, the antibody comprises a heavy chain variable domain having at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 136. See Table 4.

[0287] In some embodiments, the antibody comprises a light chain variable domain having the amino acid sequence of SEQ ID NO: 137. In some embodiments, the antibody comprises a light chain variable domain having at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 137. See Table 4.

[0288] In some embodiments, the antibody comprises a heavy chain variable domain having the amino acid sequence of SEQ ID NO: 136, and a light chain variable domain having the amino acid sequence of SEQ ID NO: 137. In some embodiments, the antibody comprises a heavy chain variable domain having at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 136, and a light chain variable domain having at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 137. See Table 4.

[0289] In some embodiments, the antibody comprises a heavy chain variable domain having the amino acid sequence of SEQ ID NO: 138. In some embodiments, the antibody comprises a heavy chain variable domain having at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 138. See Table 4.

[0290] In some embodiments, the antibody comprises a light chain variable domain having the amino acid sequence of SEQ ID NO: 139. In some embodiments, the antibody comprises a light chain variable domain having at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 139. See Table 4.

[0291] In some embodiments, the antibody comprises a heavy chain variable domain having the amino acid sequence of SEQ ID NO: 138, and a light chain variable domain having the amino acid sequence of SEQ ID NO: 139. In some embodiments, the antibody comprises a heavy chain variable domain having at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 138, and a light chain variable domain having at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 139. See Table 4.

Table 4. Heavy chain and light chain variable domain amino acid sequences of additional anti-Factor D antibodies

SEQ ID NO: 102	murine AFD Heavy Chain Variable Region	QVQLQQSGAELVKPGASVKLSCKASGYTFTSYMYWVKERPGQGLEWIGEI NPTNGGTNFNEKFKSKATLTVDTSNTAYMQLSSLTSEDSAVYYCAREGGF AYWGQGTLVTVSA
SEQ ID NO: 103	murine AFD Light Chain Variable Region	DIVMTQSQKFMSTSVGDRVSVTCKASQNVDTDVAVFQQKPGQSPRGLIYSA SSRYSGVPDRFTGSGSGTDFLTISNVQSEDLAEYFCQQYNNYPLTFGSGTK VEIK

(continued)

5	SEQ ID NO: 104	huAFD.v2.0 Heavy Chain Variable Region	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDVTSTSTAYLELSSLRSEDVAVYYCAREGGFA YWGQGTLLTVSS
10	SEQ ID NO: 105	huAFD.v2.0 Light Chain Variable Region	DIQMTQSPSSLSASVGDRVTITCKASQNVDTDVAWFQQKPGKAPKGLIYSAS SRYSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQYNLYPLTFGQGTKE IK
15	SEQ ID NO: 106	huAFD.v2.1 Heavy Chain Variable Region	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDVTSTSTAYLELSSLRSEDVAVYYCAREGGFA YWGQGTLLTVSS
20	SEQ ID NO: 107	huAFD.v2.1 Light Chain Variable Region	DIQMTQSPSSLSASVGDRVTITCKASQNVDTDVAWFQQKPGKAPKGLIRSAS SRYSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQYNLYPLTFGQGTKE IK
25	SEQ ID NO: 108	huAFD.v2.3 Heavy Chain Variable Region	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPYSGDTNFNEKFKSRATLTVDVTSTSTAYLELSSLRSEDVAVYYCAREGGFA YWGQGTLLTVSS
30	SEQ ID NO: 109	huAFD.v2.3 Light Chain Variable Region	DIQMTQSPSSLSASVGDRVTITCKASQNVDTDVAWFQQKPGKAPKGLIRSAS SRYSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQYNLYPLTFGQGTKE IK
35	SEQ ID NO: 110	huAFD.v1 Heavy Chain Variable Region	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTNGGTNFNEKFKSRATLTVDVTSTSTAYLELSSLRSEDVAVYYCAREGGF AYWGQGTLLTVSS
40	SEQ ID NO: 111	huAFD.v1 Light Chain Variable Region	DIQMTQSPSSLSASVGDRVTITCKASQNVDTDVAWFQQKPGKAPKGLIYSAS SRYSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQYNLYPLTFGQGTKE IK
45	SEQ ID NO: 112	huAFD.v1.1 Heavy Chain Variable Region	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTQGGTNFNEKFKSRATLTVDVTSTSTAYLELSSLRSEDVAVYYCAREGGF AYWGQGTLLTVSS
50	SEQ ID NO: 113	huAFD.v1.1 Light Chain Variable Region	DIQMTQSPSSLSASVGDRVTITCKASQNVDTDVAWFQQKPGKAPKGLIYSAS SRYSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQYNLYPLTFGQGTKE IK
55	SEQ ID NO: 114	huAFD.v2.2 Heavy Chain Variable Region	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGDTNFNEKFKSRATLTVDVTSTSTAYLELSSLRSEDVAVYYCAREGGFA YWGQGTLLTVSS
	SEQ ID NO: 115	huAFD.v2.2 Light Chain Variable Region	DIQMTQSPSSLSASVGDRVTITCKASQNVDTDVAWFQQKPGKAPKGLIYSAS SRYSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQYNLYPLTFGQGTKE IK

(continued)

5	SEQ ID NO: 116	huAFD.v2.4 Heavy Chain Variable Region	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDVTSTAYLELSSLRSEDVAVYYCAREGGFA YWGQGTLLTVSS
10	SEQ ID NO: 117	huAFD.v2.4 Light Chain Variable Region	DIQMTQSPSSLSASVGDRVTITCKASQNVDTDVAWFQQKPGKAPKGLIYSAS SRYSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYNNYPLTFGQGTKVE IK
15	SEQ ID NO: 118	huAFD.v2.5 Heavy Chain Variable Region	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPYSGGTNFNEKFKSRATLTVDVTSTAYLELSSLRSEDVAVYYCAREGGFA YWGQGTLLTVSS
20	SEQ ID NO: 119	huAFD.v2.5 Light Chain Variable Region	DIQMTQSPSSLSASVGDRVTITCKASQNVDTDVAWFQQKPGKAPKGLIYSAS SRYSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYNNYPLTFGQGTKVE IK
25	SEQ ID NO: 120	huAFD.v2.6 Heavy Chain Variable Region	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDVTSTAYLELSSLRSEDVAVYYCAREGGFA YWGQGTLLTVSS
30	SEQ ID NO: 121	huAFD.v2.6 Light Chain Variable Region	DIQMTQSPSSLSASVGDRVTITCKASQNVDTDVAWFQQKPGKAPKGLISSAS SRYSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYNNYPLTFGQGTKVE IK
35	SEQ ID NO: 122	huAFD.v2.7 Heavy Chain Variable Region	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDVTSTAYLELSSLRSEDVAVYYCAREGGFA YWGQGTLLTVSS
40	SEQ ID NO: 123	huAFD.v2.7 Light Chain Variable Region	DIQMTQSPSSLSASVGDRVTITCKASQNVDTDVAWFQQKPGKAPKGLIKSAS SRYSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYNNYPLTFGQGTKVE IK
45	SEQ ID NO: 124	huAFD.v2.8 Heavy Chain Variable Region	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDVTSTAYLELSSLRSEDVAVYYCAREGGFA YWGQGTLLTVSS
50	SEQ ID NO: 125	huAFD.v2.8 Light Chain Variable Region	DIQMTQSPSSLSASVGDRVTITCKASQNVDTDVAWFQQKPGKAPKGLIQSAS SRYSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYNNYPLTFGQGTKVE IK
55	SEQ ID NO: 126	huAFD.v2.9 Heavy Chain Variable Region	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIG WINPTSGGTNFNEKFKSRATLTVDVTSTAYLELSSLRSEDVAVYYCAREGG FAYWGQGTLLTVSS
	SEQ ID NO: 127	huAFD.v2.9 Light Chain Variable Region	DIQMTQSPSSLSASVGDRVTITCKASQNVDTDVAWFQQKPGKAPKGLIYSAS SRYSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYNNYPLTFGQGTKVE IK

(continued)

5	SEQ ID NO: 128	huAFD.v2.10 Heavy Chain Variable Region	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDVTSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSS
10	SEQ ID NO: 129	huAFD.v2.10 Light Chain Variable Region	DIQMTQSPSSLSASVGDRVTITCKASQNVDTDVAWFQQKPGKAPKGLIYSAS SRKSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQYNNYPLTFGQGTKVE IK
15	SEQ ID NO: 130	huAFD.v2.11 Heavy Chain Variable Region	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDVTSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSS
20	SEQ ID NO: 131	huAFD.v2.11 Light Chain Variable Region	DIQMTQSPSSLSASVGDRVTITCKASQNVDTDVAWFQQKPGKAPKGLIYSAS SRRSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQYNNYPLTFGQGTKVE IK
25	SEQ ID NO: 132	huAFD.v2.12 Heavy Chain Variable Region	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPYSGGTNFNEKFKSRATLTVDVTSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSS
30	SEQ ID NO: 133	huAFD.v2.12 Light Chain Variable Region	DIQMTQSPSSLSASVGDRVTITCKASQNVDTDVAWFQQKPGKAPKGLIRSAS SRYSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQYNNYPLTFGQGTKVE IK
35	SEQ ID NO: 134	huAFD.v2.13 Heavy Chain Variable Region	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDVTSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSS
40	SEQ ID NO: 135	huAFD.v2.13 Light Chain Variable Region	DIQMTQSPSSLSASVGDRVTITCKASQNVDTDVAWFQQKPGKAPKGLIRSAS SRYSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQYENYPLTFGQGTKVE IK
45	SEQ ID NO: 136	huAFD.v2.14 Heavy Chain Variable Region	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDVTSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSS
50	SEQ ID NO: 137	huAFD.v2.14 Light Chain Variable Region	DIQMTQSPSSLSASVGDRVTITCKASQNVDTDVAWFQQKPGKAPKGLIRSAS SRYSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQYNNYPLTFGQGTKVE IK
55	SEQ ID NO: 138	huAFD.v2.15 Heavy Chain Variable Region	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPYSGGTNFNEKFKSRATLTVDVTSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSS
	SEQ ID NO: 139	huAFD.v2.15 Light Chain Variable Region	DIQMTQSPSSLSASVGDRVTITCKASQNVDTDVAWFQQKPGKAPKGLIRSAS SRYSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQYNNYPLTFGQGTKVE IK

[0292] In some embodiments, the antibody comprises a heavy chain having the amino acid sequence of SEQ ID NO:

75, and a light chain having the amino acid sequence of SEQ ID NO: 76. In some embodiments, the antibody comprises a heavy chain having at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 75, and a light chain having at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 76. See Table 5.

[0328] In some embodiments, the antibody comprises a heavy chain having the amino acid sequence of SEQ ID NO: 77. In some embodiments, the antibody comprises a heavy chain having at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 77. See Table 5.

[0329] In some embodiments, the antibody comprises a light chain having the amino acid sequence of SEQ ID NO: 78. In some embodiments, the antibody comprises a light chain having at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 78. See Table 5.

[0330] In some embodiments, the antibody comprises a heavy chain having the amino acid sequence of SEQ ID NO: 77, and a light chain having the amino acid sequence of SEQ ID NO: 78. In some embodiments, the antibody comprises a heavy chain having at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 77, and a light chain having at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 78. See Table 5.

[0331] In some embodiments, the antibody comprises a heavy chain having the amino acid sequence of SEQ ID NO: 79. In some embodiments, the antibody comprises a heavy chain having at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 79. See Table 5.

[0332] In some embodiments, the antibody comprises a light chain having the amino acid sequence of SEQ ID NO: 80. In some embodiments, the antibody comprises a light chain having at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 80. See Table 5.

[0333] In some embodiments, the antibody comprises a heavy chain having the amino acid sequence of SEQ ID NO: 79, and a light chain having the amino acid sequence of SEQ ID NO: 80. In some embodiments, the antibody comprises a heavy chain having at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 79, and a light chain having at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 80. See Table 5.

[0334] In some embodiments, the antibody comprises a heavy chain having the amino acid sequence of SEQ ID NO: 81. In some embodiments, the antibody comprises a heavy chain having at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 81. See Table 5.

[0335] In some embodiments, the antibody comprises a light chain having the amino acid sequence of SEQ ID NO: 82. In some embodiments, the antibody comprises a light chain having at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 82. See Table 5.

[0336] In some embodiments, the antibody comprises a heavy chain having the amino acid sequence of SEQ ID NO: 81, and a light chain having the amino acid sequence of SEQ ID NO: 82. In some embodiments, the antibody comprises a heavy chain having at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 81, and a light chain having at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 82. See Table 5.

[0337] In some embodiments, the antibody comprises a heavy chain having the amino acid sequence of SEQ ID NO: 83. In some embodiments, the antibody comprises a heavy chain having at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 83. See Table 5.

[0338] In some embodiments, the antibody comprises a light chain having the amino acid sequence of SEQ ID NO: 84. In some embodiments, the antibody comprises a light chain having at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 84. See Table 5.

[0339] In some embodiments, the antibody comprises a heavy chain having the amino acid sequence of SEQ ID NO: 83, and a light chain having the amino acid sequence of SEQ ID NO: 84. In some embodiments, the antibody comprises a heavy chain having at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 83, and a light chain having at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 84. See Table 5.

Table 5. Heavy chain and light chain amino acid sequences of anti-Factor D antibodies

SEQ ID NO: 53	AFD WT Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVSLDTSVSTAYLQISLKAEDTAVVYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHT
SEQ ID NO: 54	AFD WT Light Chain	DIQVTQSPSSLASVSGDRVITITCITSTDIDDDMNWYQQKPGKVPKLLISGGNT LRPGVPSRFGSGSGTDFTLTISSLQPEDVATYYCLQSDSLPYTFGGTKVEIK RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN SQESVTEQDSKDYSLSTLTLSKADYEHKVKYACEVTHQGLSPVTKSFN RGEC

(continued)

5	SEQ ID NO: 55	AFD.v1 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFSLDTSVSTAYLQISSLKAEDTAVYYCERE GGVNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHT
10	SEQ ID NO: 56	AFD.v1 Light Chain	DIQVTQSPSSLSASVGDRVITITCITSTSIDDDMNWYQQKPGKVPKLLISGGNT LRPGVPSRFSGSGSGTDFTLTISLQPEDVATYYCLQSDSLPYTFGQGTKVEIK RTVAAPSVEFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN SQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEN
15	SEQ ID NO: 57	AFD.v2 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFSLDTSVSTAYLQISSLKAEDTAVYYCERE GGVNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHT
20	SEQ ID NO: 58	AFD.v2 Light Chain	DIQVTQSPSSLSASVGDRVITITCITSTDIEDDMNWYQQKPGKVPKLLISGGNT LRPGVPSRFSGSGSGTDFTLTISLQPEDVATYYCLQSDSLPYTFGQGTKVEIK RTVAAPSVEFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN SQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEN
25	SEQ ID NO: 59	AFD.v3 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFSLDTSVSTAYLQISSLKAEDTAVYYCERE GGVNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHT
30	SEQ ID NO: 60	AFD.v3 Light Chain	DIQVTQSPSSLSASVGDRVITITCITSTDIDSDMNWYQQKPGKVPKLLISGGNT LRPGVPSRFSGSGSGTDFTLTISLQPEDVATYYCLQSDSLPYTFGQGTKVEIK RTVAAPSVEFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN SQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEN
35	SEQ ID NO: 61	AFD.v4 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFSLDTSVSTAYLQISSLKAEDTAVYYCERE GGVNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHT
40	SEQ ID NO: 62	AFD.v4 Light Chain	DIQVTQSPSSLSASVGDRVITITCITSTDIDSDMNWYQQKPGKVPKLLISGGNT LRPGVPSRFSGSGSGTDFTLTISLQPEDVATYYCLQSDSLPYTFGQGTKVEIK RTVAAPSVEFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN SQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEN
45	SEQ ID NO: 63	AFD.v5 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFSLDTSVSTAYLQISSLKAEDTAVYYCERE GGVNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHT
50	SEQ ID NO: 64	AFD.v5 Light Chain	DIQVTQSPSSLSASVGDRVITITCITSTSIDSSMNWYQQKPGKVPKLLISGGNTL RPGVPSRFSGSGSGTDFTLTISLQPEDVATYYCLQSDSLPYTFGQGTKVEIK RTVAAPSVEFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN SQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEN
55			

EP 3 666 901 A1

(continued)

5	SEQ ID NO: 65	AFD.v6 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFSLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHT
10	SEQ ID NO: 66	AFD.v6 Light Chain	DIQVTQSPSSLSASVGDRVTTITCITSTDIESDMNWWYQQKPGKVPKLLISGGNT LRPGVPSRFGSGSGTDFTLTISLQPEDVATYYCLQSDSLPYTFGQGTKVEIK RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN SQESVTEQDSKDYSLSSLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEN
15	SEQ ID NO: 67	AFD.v7 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFSLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHT
20	SEQ ID NO: 68	AFD.v7 Light Chain	DIQVTQSPSSLSASVGDRVTTITCITSTDIESDMNWWYQQKPGKVPKLLISGGNT LRPGVPSRFGSGSGTDFTLTISLQPEDVATYYCLQSDSLPYTFGQGTKVEIK RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN SQESVTEQDSKDYSLSSLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEN
25	SEQ ID NO: 69	AFD.v8 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFSLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHT
30	SEQ ID NO: 70	AFD.v8 Light Chain	DIQVTQSPSSLSASVGDRVTTITCITSTSDIESDMNWWYQQKPGKVPKLLISGGNTL RPGVPSRFGSGSGTDFTLTISLQPEDVATYYCLQSDSLPYTFGQGTKVEIK RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN SQESVTEQDSKDYSLSSLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEN
35	SEQ ID NO: 71	AFD.v9 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFSLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHT
40	SEQ ID NO: 72	AFD.v9 Light Chain	DIQVTQSPSSLSASVGDRVTTITCITSTSDIESDMSWYQQKPGKVPKLLISGGNTL RPGVPSRFGSGSGTDFTLTISLQPEDVATYYCLQSDSLPYTFGQGTKVEIK RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN SQESVTEQDSKDYSLSSLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEN
45	SEQ ID NO: 73	AFD.v10 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFSLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHT
50	SEQ ID NO: 74	AFD.v10 Light Chain	DIQVTQSPSSLSASVGDRVTTITCITSTSDIESDMNWWYQQKPGKVPKLLISGGNTL RPGVPSRFGSGSGTDFTLTISLQPEDVATYYCLQSDSLPYTFGQGTKVEIKR TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN SQESVTEQDSKDYSLSSLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEN
55			

EP 3 666 901 A1

(continued)

5	SEQ ID NO: 75	AFD.v11 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WISTYTGETTYAEDFKGRFVFSLDTSVSTAYLQISSLKAEDTAVYYCERE GGVNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEP VTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHT
10	SEQ ID NO: 76	AFD.v11 Light Chain	DIQVTQSPSSLSASVGDRVTTITCITSTSIESDMNWDYQKPGKVPKLLISGGNTL RPGVPSRFSGSGSGTDFTLTISSLQPEDVATYYCLQSDSLPYTFGQGTKEIK RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN SQESVTEQDSKDSSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGE
15	SEQ ID NO: 77	AFD.v12 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFSLDTSVSTAYLQISSLKAEDTAVYYCERE GGVDNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEP VTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHT
20	SEQ ID NO: 78	AFD.v12 Light Chain	DIQVTQSPSSLSASVGDRVTTITCITSTSIESDMNWDYQKPGKVPKLLISGGNTL RPGVPSRFSGSGSGTDFTLTISSLQPEDVATYYCLQSDSLPYTFGQGTKEIK RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN SQESVTEQDSKDSSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGE
25	SEQ ID NO: 79	AFD.v13 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFSLDTSVSTAYLQISSLKAEDTAVYYCERE GGVQNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEP VTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHT
30	SEQ ID NO: 80	AFD.v13 Light Chain	DIQVTQSPSSLSASVGDRVTTITCITSTSIESDMNWDYQKPGKVPKLLISGGNTL RPGVPSRFSGSGSGTDFTLTISSLQPEDVATYYCLQSDSLPYTFGQGTKEIK RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN SQESVTEQDSKDSSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGE
35	SEQ ID NO: 81	AFD.v14 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFSLDTSVSTAYLQISSLKAEDTAVYYCERE GGVSNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEP VTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHT
40	SEQ ID NO: 82	AFD.v14 Light Chain	DIQVTQSPSSLSASVGDRVTTITCITSTSIESDMNWDYQKPGKVPKLLISGGNTL RPGVPSRFSGSGSGTDFTLTISSLQPEDVATYYCLQSDSLPYTFGQGTKEIK RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN SQESVTEQDSKDSSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGE
45	SEQ ID NO: 83	AFD.v15 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFSLDTSVSTAYLQISSLKAEDTAVYYCERE GGVSNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEP VTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHT
50	SEQ ID NO: 84	AFD.v15 Light Chain	DIQVTQSPSSLSASVGDRVTTITCITSTSIESDMNWDYQKPGKVPKLLISGGNTL RPGVPSRFSGSGSGTDFTLTISSLQPEDVATYYCLQSESLPYTFGQGTKEIKR TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS QESVTEQDSKDSSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGE
55			

175. In some embodiments, the antibody comprises a light chain having at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 175. See Table 6.

[0393] In some embodiments, the antibody comprises a heavy chain having the amino acid sequence of SEQ ID NO: 174, and a light chain having the amino acid sequence of SEQ ID NO: 175. In some embodiments, the antibody comprises a heavy chain having at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 174, and a light chain having at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 175. See Table 6.

Table 6. Heavy chain and light chain amino acid sequences of additional anti-Factor D antibodies

SEQ ID NO: 140	huAFD.v2.0 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFKNEFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHT
SEQ ID NO: 141	huAFD.v2.0 Light Chain	DIQMTQSPSSLSASVGDRVTITCKASQNVDTDVAWFQQKPGKAPKGLIYSAS SRYSQVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQYNNTPLTFGQGTKE IKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSG NSQESVTEQDSKSTYSLSSLTLSKADYEKHKVYACEVTHQGLSSPVTKSF NRGEC
SEQ ID NO: 142	huAFD.v2.1 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFKNEFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHT
SEQ ID NO: 143	huAFD.v2.1 Light Chain	DIQMTQSPSSLSASVGDRVTITCKASQNVDTDVAWFQQKPGKAPKGLIYSAS SRYSQVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQYNNTPLTFGQGTKE IKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSG NSQESVTEQDSKSTYSLSSLTLSKADYEKHKVYACEVTHQGLSSPVTKSF NRGEC
SEQ ID NO: 144	huAFD.v2.3 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPYSGDTNFKNEFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGF AYWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTV SWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSCDKTHT
SEQ ID NO: 145	huAFD.v2.3 Light Chain	DIQMTQSPSSLSASVGDRVTITCKASQNVDTDVAWFQQKPGKAPKGLIYSAS SRYSQVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQYNNTPLTFGQGTKE IKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSG NSQESVTEQDSKSTYSLSSLTLSKADYEKHKVYACEVTHQGLSSPVTKSF NRGEC
SEQ ID NO: 146	huAFD.v1 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTNGGTNFKNEFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGF AYWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTV SWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSCDKTHT
SEQ ID NO: 147	huAFD.v1 Light Chain	DIQMTQSPSSLSASVGDRVTITCKASQNVDTDVAWFQQKPGKAPKGLIYSAS SRYSQVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQYNNTPLTFGQGTKE IKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSG NSQESVTEQDSKSTYSLSSLTLSKADYEKHKVYACEVTHQGLSSPVTKSF NRGEC

EP 3 666 901 A1

(continued)

5	SEQ ID NO: 148	huAFD.v1.1 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTQGGTNFNEKFKSRATLTVDVTSTSTAYLELSSLRSEDTAVYYCAREGGF AYWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSCDKTHT
10	SEQ ID NO: 149	huAFD.v1.1 Light Chain	DIQMTQSPSSLSASVGDRVTITCKASQNVDTDVAWFQQKPGKAPKGLIYSAS SRYSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYNMYPLTFGQGTKVE IKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSG NSQESVTEQDSKDYSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF NRGEC
15	SEQ ID NO: 150	huAFD.v2.2 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGDTNFNEKFKSRATLTVDVTSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHT
20	SEQ ID NO: 151	huAFD.v2.2 Light Chain	DIQMTQSPSSLSASVGDRVTITCKASQNVDTDVAWFQQKPGKAPKGLIYSAS SRYSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYNMYPLTFGQGTKVE IKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSG NSQESVTEQDSKDYSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF NRGEC
25	SEQ ID NO: 152	huAFD.v2.4 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGETNFNEKFKSRATLTVDVTSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHT
30	SEQ ID NO: 153	huAFD.v2.4 Light Chain	DIQMTQSPSSLSASVGDRVTITCKASQNVDTDVAWFQQKPGKAPKGLIYSAS SRYSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYNMYPLTFGQGTKVE IKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSG NSQESVTEQDSKDYSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF NRGEC
35	SEQ ID NO: 154	huAFD.v2.5 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPYSGGTNFNEKFKSRATLTVDVTSTSTAYLELSSLRSEDTAVYYCAREGGF AYWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSCDKTHT
40	SEQ ID NO: 155	huAFD.v2.5 Light Chain	DIQMTQSPSSLSASVGDRVTITCKASQNVDTDVAWFQQKPGKAPKGLIYSAS SRYSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYNMYPLTFGQGTKVE IKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSG NSQESVTEQDSKDYSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF NRGEC
45	SEQ ID NO: 156	huAFD.v2.6 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDVTSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHT
50	SEQ ID NO: 157	huAFD.v2.6 Light Chain	DIQMTQSPSSLSASVGDRVTITCKASQNVDTDVAWFQQKPGKAPKGLISSAS SRYSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYNMYPLTFGQGTKVE IKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSG NSQESVTEQDSKDYSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF NRGEC
55			

EP 3 666 901 A1

(continued)

5	SEQ ID NO: 158	huAFD.v2.7 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFKNEKFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHT
10	SEQ ID NO: 159	huAFD.v2.7 Light Chain	DIQMTQSPSSLSASVGDRVTITCKASQNVDTDVAWFQQKPGKAPKGLIKSAS SRYSGVPSRFGSGSGTDFTLTISLQPEDFATYYCQQYNNYPLTFGQGTKVE IKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSG NSQESVTEQDSKDYSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF NRGEC
15	SEQ ID NO: 160	huAFD.v2.8 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFKNEKFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHT
20	SEQ ID NO: 161	huAFD.v2.8 Light Chain	DIQMTQSPSSLSASVGDRVTITCKASQNVDTDVAWFQQKPGKAPKGLIQSAS SRYSGVPSRFGSGSGTDFTLTISLQPEDFATYYCQQYNNYPLTFGQGTKVE IKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSG NSQESVTEQDSKDYSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF NRGEC
25	SEQ ID NO: 162	huAFD.v2.9 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIG WINPTSGGTNFKNEKFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGG FAYWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHT
30	SEQ ID NO: 163	huAFD.v2.9 Light Chain	DIQMTQSPSSLSASVGDRVTITCKASQNVDTDVAWFQQKPGKAPKGLIYSAS SRYSGVPSRFGSGSGTDFTLTISLQPEDFATYYCQQYNNYPLTFGQGTKVE IKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSG NSQESVTEQDSKDYSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF NRGEC
35	SEQ ID NO: 164	huAFD.v2.10 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFKNEKFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHT
40	SEQ ID NO: 165	huAFD.v2.10 Light Chain	DIQMTQSPSSLSASVGDRVTITCKASQNVDTDVAWFQQKPGKAPKGLIYSAS SRKSGVPSRFGSGSGTDFTLTISLQPEDFATYYCQQYNNYPLTFGQGTKVE IKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSG NSQESVTEQDSKDYSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF NRGEC
45	SEQ ID NO: 166	huAFD.v2.11 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFKNEKFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHT
50	SEQ ID NO: 167	huAFD.v2.11 Light Chain	DIQMTQSPSSLSASVGDRVTITCKASQNVDTDVAWFQQKPGKAPKGLIYSAS SRRSGVPSRFGSGSGTDFTLTISLQPEDFATYYCQQYNNYPLTFGQGTKVE IKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSG NSQESVTEQDSKDYSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF NRGEC

(continued)

5	SEQ ID NO: 168	huAFD.v2.12 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPYSGGTNFKFKSRATLTVDSTSTAYLELSSLRSEDNAVYYCAREGGF AYWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT SWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSCDKTHT
10	SEQ ID NO: 169	huAFD.v2.12 Light Chain	DIQMTQSPSSLSASVGDRVTITCKASQNVDTDVAWFQQKPGKAPKGLIRSAS SRYSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYNNYPLTFGQGTKVE IKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSG NSQESVTEQDSKDYSLSSLTLSKADYEEKHKVYACEVTHQGLSSPVTKSF NRGEC
15	SEQ ID NO: 170	huAFD.v2.13 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFKFKSRATLTVDSTSTAYLELSSLRSEDNAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHT
20	SEQ ID NO: 171	huAFD.v2.13 Light Chain	DIQMTQSPSSLSASVGDRVTITCKASQNVDTDVAWFQQKPGKAPKGLIRSAS SRYSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYNNYPLTFGQGTKVE IKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSG NSQESVTEQDSKDYSLSSLTLSKADYEEKHKVYACEVTHQGLSSPVTKSF NRGEC
25	SEQ ID NO: 172	huAFD.v2.14 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFKFKSRATLTVDSTSTAYLELSSLRSEDNAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHT
30	SEQ ID NO: 173	huAFD.v2.14 Light Chain	DIQMTQSPSSLSASVGDRVTITCKASQNVDTDVAWFQQKPGKAPKGLIRSAS SRYSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYNNYPLTFGQGTKVE IKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSG NSQESVTEQDSKDYSLSSLTLSKADYEEKHKVYACEVTHQGLSSPVTKSF NRGEC
35	SEQ ID NO: 174	huAFD.v2.15 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPYSGGTNFKFKSRATLTVDSTSTAYLELSSLRSEDNAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHT
40	SEQ ID NO: 175	huAFD.v2.15 Light Chain	DIQMTQSPSSLSASVGDRVTITCKASQNVDTDVAWFQQKPGKAPKGLIRSAS SRYSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYNNYPLTFGQGTKVE IKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSG NSQESVTEQDSKDYSLSSLTLSKADYEEKHKVYACEVTHQGLSSPVTKSF NRGEC
45			

[0394] The antibody and antigen-binding fragments described herein can also be further covalently modified by conjugating the antibody or antigen-binding fragments to one of a variety of non-proteinaceous polymer molecules. The antibody-polymer conjugates can be made using any suitable technique for derivatizing antibody with polymers, and are not limited to conjugates utilizing any particular type of linkage between an antibody or antibody fragment and a polymer.

[0395] In one aspect, the conjugates include species wherein a polymer is covalently attached to a specific site or specific sites on the parental antibody, *i.e.* polymer attachment is targeted to a particular region or a particular amino acid residue or residues in the parental antibody or antibody fragment. Site specific conjugation of polymers is most commonly achieved by attachment to cysteine residues in the parental antibody or antibody fragment. In such embodiments, the coupling chemistry can, for example, utilize the free sulfhydryl group of a cysteine residue not in a disulfide

bridge in the parental antibody. The polymer can be activated with any functional group that is capable of reacting specifically with the free sulfhydryl or thiol group(s) on the parental antibody, such as maleimide, sulfhydryl, thiol, triflate, tesylate, aziridine, oxirane, and 5-pyridyl functional groups. The polymer can be coupled to the parental antibody using any protocol suitable for the chemistry of the coupling system selected, such as the protocols and systems described

[0396] In some embodiments, one or more cysteine residue(s) naturally present in the parental antibody is (are) used as attachment site(s) for polymer conjugation. In some embodiments, one or more cysteine residue(s) is (are) engineered into a selected site or sites in the parental antibody for the purpose of providing a specific attachment site or sites for polymer. Cysteine engineered antibodies have been described previously (U.S. Pat. Pub. No. 2007/0092940 and Junutula, J. R., et al, J. Immunol Methods, Vol. 332(1-2), pp. 41-52 (2008), all herein incorporated by reference in their entirety). In some embodiments, cysteine engineered antibodies can be parental antibodies. These are useful for generating antibody fragments having a free cysteine in a particular location, typically in a constant region, e.g., CL or CH1. A parent antibody engineered to contain a cysteine may be referred to as a "ThioMab" and Fab fragments produced from such cysteine engineered antibodies, regardless of the method of production, may be referred to as "ThioMabs" or "ThioFabs." As described previously (see, e.g., U.S. Pat. Pub. No. 2007/0092940 and Junutula, J. R., et al, J. Immunol Methods, Vol. 332(1-2), pp. 41-52 (2008)), mutants with replaced ("engineered") cysteine (Cys) residues are evaluated for the reactivity of the newly introduced, engineered cysteine thiol groups. The thiol reactivity value is a relative, numerical term in the range of 0 to 1.0 and can be measured for any cysteine engineered antibody. In addition to having a reactive thiol group, ThioMabs should be selected such that they retain antigen binding capability. The design, selection, and preparation of cysteine engineered antibodies were described in detail previously (see, e.g., WO 2011/069104, which is herein incorporated by reference). Engineered cysteines are preferably introduced into the constant domains of heavy or light chains. As such, the cysteine engineered antibodies will preferably retain the antigen binding capability of their wild type, parent antibody counterparts and, as such, are capable of binding specifically, to antigens.

[0397] In one aspect, the invention encompasses antibody-polymer conjugates, wherein the antibody is a Fab fragment, and the polymer is attached to one or more cysteine residue in the light or heavy chain of the Fab fragment that would ordinarily form the inter-chain disulfide bond linking the light and heavy chains. In some embodiments, one or more cysteine residue(s) naturally present in the hinge region of the antibody is (are) used to attach the polymer. In some embodiments, one or more cysteine residues is (are) engineered into the hinge region of the Fab fragment for the purpose of providing a specific attachment site or sites for polymer.

[0398] In another aspect, the invention encompasses antibody-polymer conjugates, wherein the antibody is a Fab-C or Fab' fragment, and the polymer attachment is targeted to the hinge region of the Fab-C or Fab' fragment. In some embodiments, one or more cysteine residue(s) naturally present in the hinge region of the antibody is (are) used to attach the polymer. In some embodiments, one or more cysteine residues is (are) added to the C- terminus of the Fab fragment for the purpose of providing a specific attachment site or sites for polymer.

[0399] In another aspect, the invention encompasses antibody-polymer conjugates, wherein the antibody is a F(ab')₂ fragment, and the polymer attachment is targeted to the hinge region of the F(ab')₂ fragment. In some embodiments, one or more cysteine residue(s) naturally present in the hinge region of the antibody is (are) used to attach the polymer. In some embodiments, one or more cysteine residues is (are) engineered into the hinge region of the F(ab')₂ fragment for the purpose of providing a specific attachment site or sites for polymer.

[0400] In some embodiments, the anti-Factor D antibody (e.g., Fab fragment, Fab' fragment, or F(ab')₂ fragment) is modified by adding one cysteine at the C'-terminal end of the heavy chain for the purpose of providing one attachment site for polymer conjugation. In some embodiments, the anti-Factor D antibody (e.g., Fab fragment, Fab' fragment, or F(ab')₂ fragment) is modified by adding four additional residues, Cys-Pro-Pro-Cys, at the C'-terminal end of the heavy chain for the purpose of providing two attachment sites for polymer conjugation. In some embodiments, the anti-Factor D antibody (e.g., Fab fragment, Fab' fragment, or F(ab')₂ fragment) is modified by adding four additional residues, Cys-Pro-Pro-Ser, at the C'-terminal end of the heavy chain for the purpose of providing one attachment site for polymer conjugation. In some embodiments, the anti-Factor D antibody (e.g., Fab fragment, Fab' fragment, or F(ab')₂ fragment) is modified by adding four additional residues, Ser-Pro-Pro-Cys, at the C'-terminal end of the heavy chain for the purpose of providing one attachment site for polymer conjugation. In some embodiments, the anti-Factor D antibody (e.g., Fab fragment, Fab' fragment, or F(ab')₂ fragment) is modified by adding four additional residues, Ala-Pro-Pro-Cys, at the C'-terminal end of the heavy chain for the purpose of providing one attachment site for polymer conjugation. In some embodiments, the anti-Factor D antibody (e.g., Fab fragment, Fab' fragment, or F(ab')₂ fragment) is modified by adding four additional residues, Ser-Gly-Gly-Cys, at the C'-terminal end of the heavy chain for the purpose of providing one attachment site for polymer conjugation. In specific embodiments, the polymer conjugation is PEG polymer conjugation.

[0401] One commonly used antibody conjugation is PEGylation, wherein one or more polyethylene glycol (PEG) polymers are covalently attached to the antibody's constant region. See U.S. Pat. No. 4,179,337; 7,122,636. PEG polymers of different sizes (e.g., from about 500 D to about 300,000 D) and shapes (e.g., linear or branched) have been known and widely used in the field. The polymers useful for the present invention may be obtained commercially (e.g.,

from Nippon Oil and Fats; Nektar Therapeutics; Creative PEGWorks) or prepared from commercially available starting materials using conventional chemical procedures. PEGylation changes the physical and chemical properties of the antibody drug, and may results in improved pharmacokinetic behaviors such as improved stability, decreased immunogenicity, extended circulating life as well as increased residence time.

[0402] In some embodiments, the antibody (e.g., a Fab fragment, a Fab' fragment, a Fab-C fragment or a F(ab')₂ fragment) comprises a heavy chain having the amino acid sequence of SEQ ID NO: 176. In some embodiments, the antibody (e.g., a Fab fragment, a Fab' fragment, a Fab-C fragment or a F(ab')₂ fragment) comprises a heavy chain having at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 176. In some embodiments, the antibody (e.g., a Fab' fragment, a Fab-C fragment or a F(ab')₂ fragment) comprises a heavy chain having the amino acid sequence of SEQ ID NO: 176, wherein the cysteine at the C'Terminal end is attached to a polymer (e.g., a PEG polymer). In some embodiments, the antibody (e.g., a Fab' fragment, a Fab-C fragment or a F(ab')₂ fragment) comprises a heavy chain having at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 176, wherein the cysteine at the C'Terminal end is attached to a polymer (e.g., a PEG polymer). See Table 7.

[0403] In some embodiments, the antibody (e.g., a Fab fragment, a Fab' fragment, a Fab-C fragment or a F(ab')₂ fragment) comprises a heavy chain having the amino acid sequence of SEQ ID NO: 177. In some embodiments, the antibody (e.g., a Fab fragment, a Fab' fragment, a Fab-C fragment or a F(ab')₂ fragment) comprises a heavy chain having at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 177. In some embodiments, the antibody (e.g., a Fab' fragment, a Fab-C fragment or a F(ab')₂ fragment) comprises a heavy chain having the amino acid sequence of SEQ ID NO: 177, wherein the two cysteines in the Cys-Pro-Pro-Cys sequence at the C'Terminal end are each attached to a polymer (e.g., a PEG polymer). In some embodiments, the antibody (e.g., a Fab' fragment, a Fab-C fragment or a F(ab')₂ fragment) comprises a heavy chain having at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 177, wherein the two cysteines in the Cys-Pro-Pro-Cys sequence at the C'Terminal end are each attached to a polymer (e.g., a PEG polymer). See Table 7.

[0404] In some embodiments, the antibody (e.g., a Fab fragment, a Fab' fragment, a Fab-C fragment or a F(ab')₂ fragment) comprises a heavy chain having the amino acid sequence of SEQ ID NO: 178. In some embodiments, the antibody (e.g., a Fab fragment, a Fab' fragment, a Fab-C fragment or a F(ab')₂ fragment) comprises a heavy chain having at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 178. In some embodiments, the antibody (e.g., a Fab' fragment, a Fab-C fragment or a F(ab')₂ fragment) comprises a heavy chain having the amino acid sequence of SEQ ID NO: 178, wherein the cysteine at the C'Terminal end is attached to a polymer (e.g., a PEG polymer). In some embodiments, the antibody (e.g., a Fab' fragment, a Fab-C fragment or a F(ab')₂ fragment) comprises a heavy chain having at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 178, wherein the cysteine at the C'Terminal end is attached to a polymer (e.g., a PEG polymer). See Table 7.

[0405] In some embodiments, the antibody (e.g., a Fab fragment, a Fab' fragment, a Fab-C fragment or a F(ab')₂ fragment) comprises a heavy chain having the amino acid sequence of SEQ ID NO: 179. In some embodiments, the antibody (e.g., a Fab fragment, a Fab' fragment, a Fab-C fragment or a F(ab')₂ fragment) comprises a heavy chain having at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 179. In some embodiments, the antibody (e.g., a Fab' fragment, a Fab-C fragment or a F(ab')₂ fragment) comprises a heavy chain having the amino acid sequence of SEQ ID NO: 179, wherein the two cysteines in the Cys-Pro-Pro-Cys sequence at the C'Terminal end are each attached to a polymer (e.g., a PEG polymer). In some embodiments, the antibody (e.g., a Fab' fragment, a Fab-C fragment or a F(ab')₂ fragment) comprises a heavy chain having at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 179, wherein the two cysteines in the Cys-Pro-Pro-Cys sequence at the C'Terminal end are each attached to a polymer (e.g., a PEG polymer). See Table 7.

Table 7. Heavy chain and light chain amino acid sequences of cysteine-modified anti-Factor D antibodies

SEQ ID NO: 176	Cys-Modified AFD.v8 Heavy Chain	EVQLVQSGPELKKPGASVKVCSKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFSLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTC
SEQ ID NO: 177	Cys-Pro-Pro-Cys-Modified AFD.v8 Heavy Chain	EVQLVQSGPELKKPGASVKVCSKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFSLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTC <i>PPC</i>

(continued)

5	SEQ ID NO: 178	Cys-Modified AFD.v14 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGL VSNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTC
10	SEQ ID NO: 179	Cys-Pro-Pro- Cys-Modified AFD.v14 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGL VSNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTC <i>PPC</i>

[0406] While Fab, Fab', Fab-C and F(ab')₂ fragments provide the advantage of small size, short serum half-life, and lack of effector function, they typically include parts of the upper hinge region that can serve as neoepitopes, and are eventually recognized by the immune system and anti-hinge antibodies (AHA) are generated. These pre-existing AHA titers vary from donor to donor and may represent past and current exposure to neoepitopes. AHA can act as surrogate Fc and restore effector function of proteolytically inactivated antibodies. One reason to use a Fab, Fab', Fab-C or F(ab')₂ molecule as therapeutic format is to eliminate effector function. Thus, it is undesired to have effector function reinstated by pre-existing AHA and risk any potential safety concerns. To evade recognition by pre-existing AHAs, the Fab, Fab', Fab-C or F(ab')₂ fragments of an IgG2 or IgG4 isotype can be used. Alternatively, the heavy chain of the Fab of an IgG1 isotype can be modified to terminate with Cys-Asp or Cys-Asp-Lys-Thr-His-Leu.

[0407] In specific embodiments, the anti-Factor D antibody is a Fab fragment, a Fab' fragment, a Fab-C fragment or a F(ab')₂ fragment of an IgG2 isotype. In specific embodiments, the anti-Factor D antibody is a Fab fragment, a Fab' fragment, a Fab-C fragment or a F(ab')₂ fragment of an IgG4 isotype. In specific embodiments, the anti-Factor D antibody is a Fab fragment, a Fab' fragment, a Fab-C fragment or a F(ab')₂ fragment of an IgG1 isotype.

[0408] In specific embodiments, the anti-Factor D antibody is a Fab fragment whose C-terminal of the heavy chain is modified to terminate with Cys-Asp (CD), Cys-Asp-Lys (CDK), Cys-Asp-Lys-Thr (CDKT), Cys-Asp-Lys-Thr-His (CDKTH), Cys-Asp-Lys-Thr-His-Thr (CDKTHT), or Cys-Asp-Lys-Thr-His-Leu (CDKTHL). In specific embodiments, the anti-Factor D antibody is a Fab fragment whose C-terminal of the heavy chain is modified to terminate with Cys-Asp (CD), Cys-Asp-Lys (CDK), Cys-Asp-Lys-Thr (CDKT), Cys-Asp-Lys-Thr-His (CDKTH), or Cys-Asp-Lys-Thr-His-Leu (CDKTHL). In specific embodiments, the anti-Factor D antibody is a Fab fragment whose C-terminal of the heavy chain is modified to terminate with Cys-Asp (CD) or Cys-Asp-Lys-Thr-His-Leu (CDKTHL). In specific embodiments, the anti-Factor D antibody is a Fab fragment whose C-terminal of the heavy chain is modified to terminate with Cys-Asp-Lys-Thr-His-X (CDKTHX), wherein X is any amino acid except Thr (T). The cysteine residue(s) may be attached to a polymer (e.g., a PEG polymer). In specific embodiments, the anti-Factor D antibody is a Fab fragment of an IgG1 isotype.

[0409] In specific embodiments, the anti-Factor D antibody is a Fab-C fragment whose C-terminal of the heavy chain is modified to terminate with Cys-Asp-Lys-Thr-His-Thr-Cys (CDKTHTC). In specific embodiments, the anti-Factor D antibody is a Fab fragment, a Fab' fragment or a F(ab')₂ fragment whose C-terminal of the heavy chain is modified to terminate with Cys-Asp-Lys-Thr-His-Thr-Cys-Pro-Pro-Cys (CDKTHTCPPC), Cys-Asp-Lys-Thr-His-Thr-Cys-Pro-Pro-Ser (CDKTHTCPPS), Cys-Asp-Lys-Thr-His-Thr-Ser-Pro-Pro-Cys (CDKTHTSPPC), Cys-Asp-Lys-Thr-His-Thr-Ala-Pro-Pro-Cys (CDKTHTAPPC), or Cys-Asp-Lys-Thr-His-Thr-Ser-Gly-Gly-Cys (CDKTHTSGGC). In specific embodiments, the anti-Factor D antibody is a Fab fragment whose C-terminal of the heavy chain is modified to terminate with Cys-Tyr-Gly-Pro-Pro-Cys (CYGPPC). One, two, or three of the cysteine residue(s) (as the case may be) may each be attached to a polymer (e.g., a PEG polymer). In specific embodiments, the anti-Factor D antibody is a Fab fragment, a Fab' fragment, a Fab-C fragment or a F(ab')₂ fragment of an IgG1 isotype.

[0410] In specific embodiments, the anti-Factor D antibody is a Fab fragment whose C-terminal of the heavy chain is modified to terminate with Val-Glu-Arg-Lys (VERK). In specific embodiments, the anti-Factor D antibody is a Fab-C fragment whose C-terminal of the heavy chain is modified to terminate with Val-Glu-Arg-Lys-Cys (VERKC). The cysteine residue may be attached to a polymer (e.g., a PEG polymer). In specific embodiments, the anti-Factor D antibody is a Fab fragment or a Fab-C fragment of an IgG2 isotype.

[0411] In specific embodiments, the anti-Factor D antibody is a Fab fragment whose C-terminal of the heavy chain is modified to terminate with Lys-Tyr-Gly-Pro-Pro (KYGPP), Lys-Tyr-Gly-Pro (KYGP), Lys-Tyr-Gly (KYG), Lys-Tyr (KY), or Lys (K). In specific embodiments, the anti-Factor D antibody is a Fab-C fragment whose C-terminal of the heavy chain is modified to terminate with Lys-Tyr-Gly-Pro-Pro-Cys (KYGPPC). The cysteine residue may be attached to a polymer (e.g., a PEG polymer). In specific embodiments, the anti-Factor D antibody is a Fab fragment or a Fab-C fragment of an IgG4 isotype.

8. In specific embodiments, the Fab fragment is of an IgG1 isotype. In specific embodiments, the cysteine in the Cys-Asp-Lys-Thr (CDKT) sequence at the C' Terminal end is attached to a polymer (e.g., a PEG polymer).

[0416] In some embodiments, the anti-Factor D antibody is a Fab fragment comprising a heavy chain having the amino acid sequence of SEQ ID NO: 316, SEQ ID NO: 317, SEQ ID NO: 318, SEQ ID NO: 319, SEQ ID NO: 320, SEQ ID NO: 321, SEQ ID NO: 322, SEQ ID NO: 323, SEQ ID NO: 324, SEQ ID NO: 325, SEQ ID NO: 326, SEQ ID NO: 327, SEQ ID NO: 328, SEQ ID NO: 329, SEQ ID NO: 330, SEQ ID NO: 331, SEQ ID NO: 332, SEQ ID NO: 333, SEQ ID NO: 334, SEQ ID NO: 335, SEQ ID NO: 336, SEQ ID NO: 337, SEQ ID NO: 338, SEQ ID NO: 339, SEQ ID NO: 340, SEQ ID NO: 341, SEQ ID NO: 342, SEQ ID NO: 343, SEQ ID NO: 344, SEQ ID NO: 345, SEQ ID NO: 346, SEQ ID NO: 347, SEQ ID NO: 348, or SEQ ID NO: 349. In some embodiments, the anti-Factor D antibody is a Fab fragment comprising a heavy chain having at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 316, SEQ ID NO: 317, SEQ ID NO: 318, SEQ ID NO: 319, SEQ ID NO: 320, SEQ ID NO: 321, SEQ ID NO: 322, SEQ ID NO: 323, SEQ ID NO: 324, SEQ ID NO: 325, SEQ ID NO: 326, SEQ ID NO: 327, SEQ ID NO: 328, SEQ ID NO: 329, SEQ ID NO: 330, SEQ ID NO: 331, SEQ ID NO: 332, SEQ ID NO: 333, SEQ ID NO: 334, SEQ ID NO: 335, SEQ ID NO: 336, SEQ ID NO: 337, SEQ ID NO: 338, SEQ ID NO: 339, SEQ ID NO: 340, SEQ ID NO: 341, SEQ ID NO: 342, SEQ ID NO: 343, SEQ ID NO: 344, SEQ ID NO: 345, SEQ ID NO: 346, SEQ ID NO: 347, SEQ ID NO: 348, or SEQ ID NO: 349. See Table 8. In specific embodiments, the Fab fragment is of an IgG1 isotype. In specific embodiments, the cysteine in the Cys-Asp-Lys-Thr-His (CDKTH) sequence at the C' Terminal end is attached to a polymer (e.g., a PEG polymer).

[0417] In some embodiments, the anti-Factor D antibody is a Fab-C fragment comprising a heavy chain having the amino acid sequence of SEQ ID NO: 350, SEQ ID NO: 351, SEQ ID NO: 352, SEQ ID NO: 353, SEQ ID NO: 354, SEQ ID NO: 355, SEQ ID NO: 356, SEQ ID NO: 357, SEQ ID NO: 358, SEQ ID NO: 359, SEQ ID NO: 360, SEQ ID NO: 361, SEQ ID NO: 362, SEQ ID NO: 363, SEQ ID NO: 364, SEQ ID NO: 365, SEQ ID NO: 366, SEQ ID NO: 367, SEQ ID NO: 368, SEQ ID NO: 369, SEQ ID NO: 370, SEQ ID NO: 371, SEQ ID NO: 372, SEQ ID NO: 373, SEQ ID NO: 374, SEQ ID NO: 375, SEQ ID NO: 376, SEQ ID NO: 377, SEQ ID NO: 378, SEQ ID NO: 379, SEQ ID NO: 380, SEQ ID NO: 381, SEQ ID NO: 382, or SEQ ID NO: 383. In some embodiments, the anti-Factor D antibody is a Fab-C fragment comprising a heavy chain having at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 350, SEQ ID NO: 351, SEQ ID NO: 352, SEQ ID NO: 353, SEQ ID NO: 354, SEQ ID NO: 355, SEQ ID NO: 356, SEQ ID NO: 357, SEQ ID NO: 358, SEQ ID NO: 359, SEQ ID NO: 360, SEQ ID NO: 361, SEQ ID NO: 362, SEQ ID NO: 363, SEQ ID NO: 364, SEQ ID NO: 365, SEQ ID NO: 366, SEQ ID NO: 367, SEQ ID NO: 368, SEQ ID NO: 369, SEQ ID NO: 370, SEQ ID NO: 371, SEQ ID NO: 372, SEQ ID NO: 373, SEQ ID NO: 374, SEQ ID NO: 375, SEQ ID NO: 376, SEQ ID NO: 377, SEQ ID NO: 378, SEQ ID NO: 379, SEQ ID NO: 380, SEQ ID NO: 381, SEQ ID NO: 382, or SEQ ID NO: 383. See Table 8. In specific embodiments, the Fab-C fragment is of an IgG1 isotype. In specific embodiments, the two cysteines in the Cys-Asp-Lys-Thr-His-Thr-Cys (CDKTHTC) sequence at the C' Terminal end are each attached to a polymer (e.g., a PEG polymer). In specific embodiments, the first cysteine in the Cys-Asp-Lys-Thr-His-Thr-Cys (CDKTHTC) sequence at the C' Terminal end is attached to a polymer (e.g., a PEG polymer). In specific embodiments, the second cysteine in the Cys-Asp-Lys-Thr-His-Thr-Cys (CDKTHTC) sequence at the C' Terminal end is attached to a polymer (e.g., a PEG polymer).

[0418] In some embodiments, the anti-Factor D antibody is a Fab fragment, a Fab' fragment or a F(ab')₂ fragment comprising a heavy chain having the amino acid sequence of SEQ ID NO: 384, SEQ ID NO: 385, SEQ ID NO: 386, SEQ ID NO: 387, SEQ ID NO: 388, SEQ ID NO: 389, SEQ ID NO: 390, SEQ ID NO: 391, SEQ ID NO: 392, SEQ ID NO: 393, SEQ ID NO: 394, SEQ ID NO: 395, SEQ ID NO: 396, SEQ ID NO: 397, SEQ ID NO: 398, SEQ ID NO: 399, SEQ ID NO: 400, SEQ ID NO: 401, SEQ ID NO: 402, SEQ ID NO: 403, SEQ ID NO: 404, SEQ ID NO: 405, SEQ ID NO: 406, SEQ ID NO: 407, SEQ ID NO: 408, SEQ ID NO: 409, SEQ ID NO: 410, SEQ ID NO: 411, SEQ ID NO: 412, SEQ ID NO: 413, SEQ ID NO: 414, SEQ ID NO: 415, SEQ ID NO: 416, or SEQ ID NO: 417. In some embodiments, the anti-Factor D antibody is a Fab fragment, a Fab' fragment or a F(ab')₂ fragment comprising a heavy chain having at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 384, SEQ ID NO: 385, SEQ ID NO: 386, SEQ ID NO: 387, SEQ ID NO: 388, SEQ ID NO: 389, SEQ ID NO: 390, SEQ ID NO: 391, SEQ ID NO: 392, SEQ ID NO: 393, SEQ ID NO: 394, SEQ ID NO: 395, SEQ ID NO: 396, SEQ ID NO: 397, SEQ ID NO: 398, SEQ ID NO: 399, SEQ ID NO: 400, SEQ ID NO: 401, SEQ ID NO: 402, SEQ ID NO: 403, SEQ ID NO: 404, SEQ ID NO: 405, SEQ ID NO: 406, SEQ ID NO: 407, SEQ ID NO: 408, SEQ ID NO: 409, SEQ ID NO: 410, SEQ ID NO: 411, SEQ ID NO: 412, SEQ ID NO: 413, SEQ ID NO: 414, SEQ ID NO: 415, SEQ ID NO: 416, or SEQ ID NO: 417. See Table 8. In specific embodiments, the Fab fragment, Fab' fragment or F(ab')₂ fragment is of an IgG1 isotype. In specific embodiments, the three cysteines in the Cys-Asp-Lys-Thr-His-Thr-Cys-Pro-Pro-Cys (CDKTHTCPPC) sequence at the C' Terminal end are each attached to a polymer (e.g., a PEG polymer). In specific embodiments, the second cysteine and the third cysteine in the Cys-Asp-Lys-Thr-His-Thr-Cys-Pro-Pro-Cys (CDKTHTCPPC) sequence at the C' Terminal end are each attached to a polymer (e.g., a PEG polymer). In specific embodiments, the first cysteine and the third cysteine in the Cys-Asp-Lys-Thr-His-Thr-Cys-Pro-Pro-Cys (CDKTHTCPPC) sequence at the C' Terminal end are each attached to a polymer (e.g., a PEG polymer). In specific embodiments, the first cysteine and the second cysteine in the Cys-Asp-Lys-Thr-His-Thr-Cys-Pro-Pro-Cys (CDKTHTCPPC) sequence at the C' Terminal end are each attached to a polymer (e.g., a PEG polymer). In

specific embodiments, the first cysteine in the Cys-Asp-Lys-Thr-His-Thr-Cys-Pro-Pro-Cys (CDKTHTCPPC) sequence at the C' Terminal end is attached to a polymer (e.g., a PEG polymer). In specific embodiments, the second cysteine in the Cys-Asp-Lys-Thr-His-Thr-Cys-Pro-Pro-Cys (CDKTHTCPPC) sequence at the C' Terminal end is attached to a polymer (e.g., a PEG polymer). In specific embodiments, the third cysteine in the Cys-Asp-Lys-Thr-His-Thr-Cys-Pro-Pro-Cys (CDKTHTCPPC) sequence at the C' Terminal end is attached to a polymer (e.g., a PEG polymer).

[0419] In some embodiments, the anti-Factor D antibody is a Fab fragment, a Fab' fragment or a F(ab')₂ fragment comprising a heavy chain having the amino acid sequence of SEQ ID NO: 418, SEQ ID NO: 419, SEQ ID NO: 420, SEQ ID NO: 421, SEQ ID NO: 422, SEQ ID NO: 423, SEQ ID NO: 424, SEQ ID NO: 425, SEQ ID NO: 426, SEQ ID NO: 427, SEQ ID NO: 428, SEQ ID NO: 429, SEQ ID NO: 430, SEQ ID NO: 431, SEQ ID NO: 432, SEQ ID NO: 433, SEQ ID NO: 434, SEQ ID NO: 435, SEQ ID NO: 436, SEQ ID NO: 437, SEQ ID NO: 438, SEQ ID NO: 439, SEQ ID NO: 440, SEQ ID NO: 441, SEQ ID NO: 442, SEQ ID NO: 443, SEQ ID NO: 444, SEQ ID NO: 445, SEQ ID NO: 446, SEQ ID NO: 447, SEQ ID NO: 448, SEQ ID NO: 449, SEQ ID NO: 450, or SEQ ID NO: 451. In some embodiments, the anti-Factor D antibody is a Fab fragment, a Fab' fragment or a F(ab')₂ fragment comprising a heavy chain having at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 418, SEQ ID NO: 419, SEQ ID NO: 420, SEQ ID NO: 421, SEQ ID NO: 422, SEQ ID NO: 423, SEQ ID NO: 424, SEQ ID NO: 425, SEQ ID NO: 426, SEQ ID NO: 427, SEQ ID NO: 428, SEQ ID NO: 429, SEQ ID NO: 430, SEQ ID NO: 431, SEQ ID NO: 432, SEQ ID NO: 433, SEQ ID NO: 434, SEQ ID NO: 435, SEQ ID NO: 436, SEQ ID NO: 437, SEQ ID NO: 438, SEQ ID NO: 439, SEQ ID NO: 440, SEQ ID NO: 441, SEQ ID NO: 442, SEQ ID NO: 443, SEQ ID NO: 444, SEQ ID NO: 445, SEQ ID NO: 446, SEQ ID NO: 447, SEQ ID NO: 448, SEQ ID NO: 449, SEQ ID NO: 450, or SEQ ID NO: 451. See Table 8. In specific embodiments, the Fab fragment, Fab' fragment or F(ab')₂ fragment is of an IgG1 isotype. In specific embodiments, the two cysteines in the Cys-Asp-Lys-Thr-His-Thr-Cys-Pro-Pro-Ser (CDKTHTCPPS) sequence at the C' Terminal end are each attached to a polymer (e.g., a PEG polymer). In specific embodiments, the first cysteine in the Cys-Asp-Lys-Thr-His-Thr-Cys-Pro-Pro-Ser (CDKTHTCPPS) sequence at the C' Terminal end is attached to a polymer (e.g., a PEG polymer). In specific embodiments, the second cysteine in the Cys-Asp-Lys-Thr-His-Thr-Cys-Pro-Pro-Ser (CDKTHTCPPS) sequence at the C' Terminal end is attached to a polymer (e.g., a PEG polymer).

[0420] In some embodiments, the anti-Factor D antibody is a Fab fragment, a Fab' fragment or a F(ab')₂ fragment comprising a heavy chain having the amino acid sequence of SEQ ID NO: 452, SEQ ID NO: 453, SEQ ID NO: 454, SEQ ID NO: 455, SEQ ID NO: 456, SEQ ID NO: 457, SEQ ID NO: 458, SEQ ID NO: 459, SEQ ID NO: 460, SEQ ID NO: 461, SEQ ID NO: 462, SEQ ID NO: 463, SEQ ID NO: 464, SEQ ID NO: 465, SEQ ID NO: 466, SEQ ID NO: 467, SEQ ID NO: 468, SEQ ID NO: 469, SEQ ID NO: 470, SEQ ID NO: 471, SEQ ID NO: 472, SEQ ID NO: 473, SEQ ID NO: 474, SEQ ID NO: 475, SEQ ID NO: 476, SEQ ID NO: 477, SEQ ID NO: 478, SEQ ID NO: 479, SEQ ID NO: 480, SEQ ID NO: 481, SEQ ID NO: 482, SEQ ID NO: 483, SEQ ID NO: 484, or SEQ ID NO: 485. In some embodiments, the anti-Factor D antibody is a Fab fragment, a Fab' fragment or a F(ab')₂ fragment comprising a heavy chain having at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 452, SEQ ID NO: 453, SEQ ID NO: 454, SEQ ID NO: 455, SEQ ID NO: 456, SEQ ID NO: 457, SEQ ID NO: 458, SEQ ID NO: 459, SEQ ID NO: 460, SEQ ID NO: 461, SEQ ID NO: 462, SEQ ID NO: 463, SEQ ID NO: 464, SEQ ID NO: 465, SEQ ID NO: 466, SEQ ID NO: 467, SEQ ID NO: 468, SEQ ID NO: 469, SEQ ID NO: 470, SEQ ID NO: 471, SEQ ID NO: 472, SEQ ID NO: 473, SEQ ID NO: 474, SEQ ID NO: 475, SEQ ID NO: 476, SEQ ID NO: 477, SEQ ID NO: 478, SEQ ID NO: 479, SEQ ID NO: 480, SEQ ID NO: 481, SEQ ID NO: 482, SEQ ID NO: 483, SEQ ID NO: 484, or SEQ ID NO: 485. See Table 8. In specific embodiments, the Fab fragment, Fab' fragment or F(ab')₂ fragment is of an IgG1 isotype. In specific embodiments, the two cysteines in the Cys-Asp-Lys-Thr-His-Thr-Ser-Pro-Pro-Cys (CDKHTSPPC) sequence at the C' Terminal end are each attached to a polymer (e.g., a PEG polymer). In specific embodiments, the first cysteine in the Cys-Asp-Lys-Thr-His-Thr-Ser-Pro-Pro-Cys (CDKHTSPPC) sequence at the C' Terminal end is attached to a polymer (e.g., a PEG polymer). In specific embodiments, the second cysteine in the Cys-Asp-Lys-Thr-His-Thr-Ser-Pro-Pro-Cys (CDKHTSPPC) sequence at the C' Terminal end is attached to a polymer (e.g., a PEG polymer).

[0421] In some embodiments, the anti-Factor D antibody is a Fab fragment, a Fab' fragment or a F(ab')₂ fragment comprising a heavy chain having the amino acid sequence of SEQ ID NO: 486, SEQ ID NO: 487, SEQ ID NO: 488, SEQ ID NO: 489, SEQ ID NO: 490, SEQ ID NO: 491, SEQ ID NO: 492, SEQ ID NO: 493, SEQ ID NO: 494, SEQ ID NO: 495, SEQ ID NO: 496, SEQ ID NO: 497, SEQ ID NO: 498, SEQ ID NO: 499, SEQ ID NO: 500, SEQ ID NO: 501, SEQ ID NO: 502, SEQ ID NO: 503, SEQ ID NO: 504, SEQ ID NO: 505, SEQ ID NO: 506, SEQ ID NO: 507, SEQ ID NO: 508, SEQ ID NO: 509, SEQ ID NO: 510, SEQ ID NO: 511, SEQ ID NO: 512, SEQ ID NO: 513, SEQ ID NO: 514, SEQ ID NO: 515, SEQ ID NO: 516, SEQ ID NO: 517, SEQ ID NO: 518, or SEQ ID NO: 519. In some embodiments, the anti-Factor D antibody is a Fab fragment, a Fab' fragment or a F(ab')₂ fragment comprising a heavy chain having at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 486, SEQ ID NO: 487, SEQ ID NO: 488, SEQ ID NO: 489, SEQ ID NO: 490, SEQ ID NO: 491, SEQ ID NO: 492, SEQ ID NO: 493, SEQ ID NO: 494, SEQ ID NO: 495, SEQ ID NO: 496, SEQ ID NO: 497, SEQ ID NO: 498, SEQ ID NO: 499, SEQ ID NO: 500, SEQ ID NO: 501, SEQ ID NO: 502, SEQ ID NO: 503, SEQ ID NO: 504, SEQ ID NO: 505, SEQ ID NO: 506, SEQ ID NO: 507, SEQ ID NO: 508, SEQ ID NO: 509, SEQ ID NO: 510, SEQ ID NO: 511, SEQ ID NO: 512, SEQ ID NO: 513, SEQ ID NO: 514, SEQ ID

NO: 515, SEQ ID NO: 516, SEQ ID NO: 517, SEQ ID NO: 518, or SEQ ID NO: 519. See Table 8. In specific embodiments, the Fab fragment, Fab' fragment or F(ab')₂ fragment is of an IgG1 isotype. In specific embodiments, the two cysteines in the Cys-Asp-Lys-Thr-His-Thr-Ala-Pro-Pro-Cys (CDKTHTAPPC) sequence at the C' Terminal end are each attached to a polymer (e.g., a PEG polymer). In specific embodiments, the first cysteine in the Cys-Asp-Lys-Thr-His-Thr-Ala-Pro-Pro-Cys (CDKTHTAPPC) sequence at the C' Terminal end is attached to a polymer (e.g., a PEG polymer). In specific embodiments, the second cysteine in the Cys-Asp-Lys-Thr-His-Thr-Ala-Pro-Pro-Cys (CDKTHTAPPC) sequence at the C' Terminal end is attached to a polymer (e.g., a PEG polymer).

[0422] In some embodiments, the anti-Factor D antibody is a Fab fragment, a Fab' fragment or a F(ab')₂ fragment comprising a heavy chain having the amino acid sequence of SEQ ID NO: 520, SEQ ID NO: 521, SEQ ID NO: 522, SEQ ID NO: 523, SEQ ID NO: 524, SEQ ID NO: 525, SEQ ID NO: 526, SEQ ID NO: 527, SEQ ID NO: 528, SEQ ID NO: 529, SEQ ID NO: 530, SEQ ID NO: 531, SEQ ID NO: 532, SEQ ID NO: 533, SEQ ID NO: 534, SEQ ID NO: 535, SEQ ID NO: 536, SEQ ID NO: 537, SEQ ID NO: 538, SEQ ID NO: 539, SEQ ID NO: 540, SEQ ID NO: 541, SEQ ID NO: 542, SEQ ID NO: 543, SEQ ID NO: 544, SEQ ID NO: 545, SEQ ID NO: 546, SEQ ID NO: 547, SEQ ID NO: 548, SEQ ID NO: 549, SEQ ID NO: 550, SEQ ID NO: 551, SEQ ID NO: 552, or SEQ ID NO: 553. In some embodiments, the anti-Factor D antibody is a Fab fragment, a Fab' fragment or a F(ab')₂ fragment comprising a heavy chain having at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 520, SEQ ID NO: 521, SEQ ID NO: 522, SEQ ID NO: 523, SEQ ID NO: 524, SEQ ID NO: 525, SEQ ID NO: 526, SEQ ID NO: 527, SEQ ID NO: 528, SEQ ID NO: 529, SEQ ID NO: 530, SEQ ID NO: 531, SEQ ID NO: 532, SEQ ID NO: 533, SEQ ID NO: 534, SEQ ID NO: 535, SEQ ID NO: 536, SEQ ID NO: 537, SEQ ID NO: 538, SEQ ID NO: 539, SEQ ID NO: 540, SEQ ID NO: 541, SEQ ID NO: 542, SEQ ID NO: 543, SEQ ID NO: 544, SEQ ID NO: 545, SEQ ID NO: 546, SEQ ID NO: 547, SEQ ID NO: 548, SEQ ID NO: 549, SEQ ID NO: 550, SEQ ID NO: 551, SEQ ID NO: 552, or SEQ ID NO: 553. See Table 8. In specific embodiments, the Fab fragment, Fab' fragment or F(ab')₂ fragment is of an IgG1 isotype. In specific embodiments, the two cysteines in the Cys-Asp-Lys-Thr-His-Thr-Ser-Gly-Gly-Cys (CDKHTSGGC) sequence at the C' Terminal end are each attached to a polymer (e.g., a PEG polymer). In specific embodiments, the first cysteine in the Cys-Asp-Lys-Thr-His-Thr-Ser-Gly-Gly-Cys (CDKHTSGGC) sequence at the C' Terminal end is attached to a polymer (e.g., a PEG polymer). In specific embodiments, the second cysteine in the Cys-Asp-Lys-Thr-His-Thr-Ser-Gly-Gly-Cys (CDKHTSGGC) sequence at the C' Terminal end is attached to a polymer (e.g., a PEG polymer).

[0423] In some embodiments, the anti-Factor D antibody is a Fab fragment comprising a heavy chain having the amino acid sequence of SEQ ID NO: 554, SEQ ID NO: 555, SEQ ID NO: 556, SEQ ID NO: 557, SEQ ID NO: 558, SEQ ID NO: 559, SEQ ID NO: 560, SEQ ID NO: 561, SEQ ID NO: 562, SEQ ID NO: 563, SEQ ID NO: 564, SEQ ID NO: 565, SEQ ID NO: 566, SEQ ID NO: 567, SEQ ID NO: 568, SEQ ID NO: 569, SEQ ID NO: 570, SEQ ID NO: 571, SEQ ID NO: 572, SEQ ID NO: 573, SEQ ID NO: 574, SEQ ID NO: 575, SEQ ID NO: 576, SEQ ID NO: 577, SEQ ID NO: 578, SEQ ID NO: 579, SEQ ID NO: 580, SEQ ID NO: 581, SEQ ID NO: 582, SEQ ID NO: 583, SEQ ID NO: 584, SEQ ID NO: 585, SEQ ID NO: 586, or SEQ ID NO: 587. In some embodiments, the anti-Factor D antibody is a Fab fragment comprising a heavy chain having at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 554, SEQ ID NO: 555, SEQ ID NO: 556, SEQ ID NO: 557, SEQ ID NO: 558, SEQ ID NO: 559, SEQ ID NO: 560, SEQ ID NO: 561, SEQ ID NO: 562, SEQ ID NO: 563, SEQ ID NO: 564, SEQ ID NO: 565, SEQ ID NO: 566, SEQ ID NO: 567, SEQ ID NO: 568, SEQ ID NO: 569, SEQ ID NO: 570, SEQ ID NO: 571, SEQ ID NO: 572, SEQ ID NO: 573, SEQ ID NO: 574, SEQ ID NO: 575, SEQ ID NO: 576, SEQ ID NO: 577, SEQ ID NO: 578, SEQ ID NO: 579, SEQ ID NO: 580, SEQ ID NO: 581, SEQ ID NO: 582, SEQ ID NO: 583, SEQ ID NO: 584, SEQ ID NO: 585, SEQ ID NO: 586, or SEQ ID NO: 587. See Table 8. In specific embodiments, the Fab fragment is of an IgG1 isotype. In specific embodiments, the two cysteines in the Cys-Tyr-Gly-Pro-Pro-Cys (CYGPPC) sequence at the C' Terminal end are each attached to a polymer (e.g., a PEG polymer). In specific embodiments, the first cysteine in the Cys-Tyr-Gly-Pro-Pro-Cys (CYGPPC) sequence at the C' Terminal end is attached to a polymer (e.g., a PEG polymer). In specific embodiments, the second cysteine in the Cys-Tyr-Gly-Pro-Pro-Cys (CYGPPC) sequence at the C' Terminal end is attached to a polymer (e.g., a PEG polymer).

[0424] In some embodiments, the anti-Factor D antibody is a Fab fragment comprising a heavy chain having the amino acid sequence of SEQ ID NO: 588, SEQ ID NO: 589, SEQ ID NO: 590, SEQ ID NO: 591, SEQ ID NO: 592, SEQ ID NO: 593, SEQ ID NO: 594, SEQ ID NO: 595, SEQ ID NO: 596, SEQ ID NO: 597, SEQ ID NO: 598, SEQ ID NO: 599, SEQ ID NO: 600, SEQ ID NO: 601, SEQ ID NO: 602, SEQ ID NO: 603, SEQ ID NO: 604, SEQ ID NO: 605, SEQ ID NO: 606, SEQ ID NO: 607, SEQ ID NO: 608, SEQ ID NO: 609, SEQ ID NO: 610, SEQ ID NO: 611, SEQ ID NO: 612, SEQ ID NO: 613, SEQ ID NO: 614, SEQ ID NO: 615, SEQ ID NO: 616, SEQ ID NO: 617, SEQ ID NO: 618, SEQ ID NO: 619, SEQ ID NO: 620, or SEQ ID NO: 621. In some embodiments, the anti-Factor D antibody is a Fab fragment comprising a heavy chain having at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 588, SEQ ID NO: 589, SEQ ID NO: 590, SEQ ID NO: 591, SEQ ID NO: 592, SEQ ID NO: 593, SEQ ID NO: 594, SEQ ID NO: 595, SEQ ID NO: 596, SEQ ID NO: 597, SEQ ID NO: 598, SEQ ID NO: 599, SEQ ID NO: 600, SEQ ID NO: 601, SEQ ID NO: 602, SEQ ID NO: 603, SEQ ID NO: 604, SEQ ID NO: 605, SEQ ID NO: 606, SEQ ID NO: 607, SEQ ID NO: 608, SEQ ID NO: 609, SEQ ID NO: 610, SEQ ID NO: 611, SEQ ID NO: 612, SEQ ID NO: 613, SEQ ID NO: 614, SEQ ID NO: 615, SEQ ID NO: 616, SEQ ID NO: 617, SEQ ID NO: 618, SEQ ID NO: 619, SEQ ID NO: 620, or SEQ ID NO: 621. See Table

8. In specific embodiments, the Fab fragment is of an IgG2 isotype.

[0425] In some embodiments, the anti-Factor D antibody is a Fab-C fragment comprising a heavy chain having the amino acid sequence of SEQ ID NO: 622, SEQ ID NO: 623, SEQ ID NO: 624, SEQ ID NO: 625, SEQ ID NO: 626, SEQ ID NO: 627, SEQ ID NO: 628, SEQ ID NO: 629, SEQ ID NO: 630, SEQ ID NO: 631, SEQ ID NO: 632, SEQ ID NO: 633, SEQ ID NO: 634, SEQ ID NO: 635, SEQ ID NO: 636, SEQ ID NO: 637, SEQ ID NO: 638, SEQ ID NO: 639, SEQ ID NO: 640, SEQ ID NO: 641, SEQ ID NO: 642, SEQ ID NO: 643, SEQ ID NO: 644, SEQ ID NO: 645, SEQ ID NO: 646, SEQ ID NO: 647, SEQ ID NO: 648, SEQ ID NO: 649, SEQ ID NO: 650, SEQ ID NO: 651, SEQ ID NO: 652, SEQ ID NO: 653, SEQ ID NO: 654, or SEQ ID NO: 655. In some embodiments, the anti-Factor D antibody is a Fab-C fragment comprising a heavy chain having at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 622, SEQ ID NO: 623, SEQ ID NO: 624, SEQ ID NO: 625, SEQ ID NO: 626, SEQ ID NO: 627, SEQ ID NO: 628, SEQ ID NO: 629, SEQ ID NO: 630, SEQ ID NO: 631, SEQ ID NO: 632, SEQ ID NO: 633, SEQ ID NO: 634, SEQ ID NO: 635, SEQ ID NO: 636, SEQ ID NO: 637, SEQ ID NO: 638, SEQ ID NO: 639, SEQ ID NO: 640, SEQ ID NO: 641, SEQ ID NO: 642, SEQ ID NO: 643, SEQ ID NO: 644, SEQ ID NO: 645, SEQ ID NO: 646, SEQ ID NO: 647, SEQ ID NO: 648, SEQ ID NO: 649, SEQ ID NO: 650, SEQ ID NO: 651, SEQ ID NO: 652, SEQ ID NO: 653, SEQ ID NO: 654, or SEQ ID NO: 655. See Table 8. In specific embodiments, the Fab-C fragment is of an IgG2 isotype. In specific embodiments, the cysteine in the Val-Glu-Arg-Lys-Cys (VERKC) sequence at the C' Terminal end is attached to a polymer (e.g., a PEG polymer).

[0426] In some embodiments, the anti-Factor D antibody is a Fab-C fragment comprising a heavy chain having the amino acid sequence of SEQ ID NO: 656, SEQ ID NO: 657, SEQ ID NO: 658, SEQ ID NO: 659, SEQ ID NO: 660, SEQ ID NO: 661, SEQ ID NO: 662, SEQ ID NO: 663, SEQ ID NO: 664, SEQ ID NO: 665, SEQ ID NO: 666, SEQ ID NO: 667, SEQ ID NO: 668, SEQ ID NO: 669, SEQ ID NO: 670, SEQ ID NO: 671, SEQ ID NO: 672, SEQ ID NO: 673, SEQ ID NO: 674, SEQ ID NO: 675, SEQ ID NO: 676, SEQ ID NO: 677, SEQ ID NO: 678, SEQ ID NO: 679, SEQ ID NO: 680, SEQ ID NO: 681, SEQ ID NO: 682, SEQ ID NO: 683, SEQ ID NO: 684, SEQ ID NO: 685, SEQ ID NO: 686, SEQ ID NO: 687, SEQ ID NO: 688, or SEQ ID NO: 689. In some embodiments, the anti-Factor D antibody is a Fab-C fragment comprising a heavy chain having at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 656, SEQ ID NO: 657, SEQ ID NO: 658, SEQ ID NO: 659, SEQ ID NO: 660, SEQ ID NO: 661, SEQ ID NO: 662, SEQ ID NO: 663, SEQ ID NO: 664, SEQ ID NO: 665, SEQ ID NO: 666, SEQ ID NO: 667, SEQ ID NO: 668, SEQ ID NO: 669, SEQ ID NO: 670, SEQ ID NO: 671, SEQ ID NO: 672, SEQ ID NO: 673, SEQ ID NO: 674, SEQ ID NO: 675, SEQ ID NO: 676, SEQ ID NO: 677, SEQ ID NO: 678, SEQ ID NO: 679, SEQ ID NO: 680, SEQ ID NO: 681, SEQ ID NO: 682, SEQ ID NO: 683, SEQ ID NO: 684, SEQ ID NO: 685, SEQ ID NO: 686, SEQ ID NO: 687, SEQ ID NO: 688, or SEQ ID NO: 689. See Table 8. In specific embodiments, the Fab-C fragment is of an IgG4 isotype. In specific embodiments, the cysteine in the Lys-Tyr-Gly-Pro-Pro-Cys (KYGPPC) sequence at the C' Terminal end is attached to a polymer (e.g., a PEG polymer).

[0427] In some embodiments, the anti-Factor D antibody is a Fab fragment comprising a heavy chain having the amino acid sequence of SEQ ID NO: 690, SEQ ID NO: 691, SEQ ID NO: 692, SEQ ID NO: 693, SEQ ID NO: 694, SEQ ID NO: 695, SEQ ID NO: 696, SEQ ID NO: 697, SEQ ID NO: 698, SEQ ID NO: 699, SEQ ID NO: 700, SEQ ID NO: 701, SEQ ID NO: 702, SEQ ID NO: 703, SEQ ID NO: 704, SEQ ID NO: 705, SEQ ID NO: 706, SEQ ID NO: 707, SEQ ID NO: 708, SEQ ID NO: 709, SEQ ID NO: 710, SEQ ID NO: 711, SEQ ID NO: 712, SEQ ID NO: 713, SEQ ID NO: 714, SEQ ID NO: 715, SEQ ID NO: 716, SEQ ID NO: 717, SEQ ID NO: 718, SEQ ID NO: 719, SEQ ID NO: 720, SEQ ID NO: 721, SEQ ID NO: 722, or SEQ ID NO: 723. In some embodiments, the anti-Factor D antibody is a Fab fragment comprising a heavy chain having at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 690, SEQ ID NO: 691, SEQ ID NO: 692, SEQ ID NO: 693, SEQ ID NO: 694, SEQ ID NO: 695, SEQ ID NO: 696, SEQ ID NO: 697, SEQ ID NO: 698, SEQ ID NO: 699, SEQ ID NO: 700, SEQ ID NO: 701, SEQ ID NO: 702, SEQ ID NO: 703, SEQ ID NO: 704, SEQ ID NO: 705, SEQ ID NO: 706, SEQ ID NO: 707, SEQ ID NO: 708, SEQ ID NO: 709, SEQ ID NO: 710, SEQ ID NO: 711, SEQ ID NO: 712, SEQ ID NO: 713, SEQ ID NO: 714, SEQ ID NO: 715, SEQ ID NO: 716, SEQ ID NO: 717, SEQ ID NO: 718, SEQ ID NO: 719, SEQ ID NO: 720, SEQ ID NO: 721, SEQ ID NO: 722, or SEQ ID NO: 723. See Table 8. In specific embodiments, the Fab fragment is of an IgG4 isotype.

[0428] In some embodiments, the anti-Factor D antibody is a Fab fragment comprising a heavy chain having the amino acid sequence of SEQ ID NO: 724, SEQ ID NO: 725, SEQ ID NO: 726, SEQ ID NO: 727, SEQ ID NO: 728, SEQ ID NO: 729, SEQ ID NO: 730, SEQ ID NO: 731, SEQ ID NO: 732, SEQ ID NO: 733, SEQ ID NO: 734, SEQ ID NO: 735, SEQ ID NO: 736, SEQ ID NO: 737, SEQ ID NO: 738, SEQ ID NO: 739, SEQ ID NO: 740, SEQ ID NO: 741, SEQ ID NO: 742, SEQ ID NO: 743, SEQ ID NO: 744, SEQ ID NO: 745, SEQ ID NO: 746, SEQ ID NO: 747, SEQ ID NO: 748, SEQ ID NO: 749, SEQ ID NO: 750, SEQ ID NO: 751, SEQ ID NO: 752, SEQ ID NO: 753, SEQ ID NO: 754, SEQ ID NO: 755, SEQ ID NO: 756, or SEQ ID NO: 757. In some embodiments, the anti-Factor D antibody is a Fab fragment comprising a heavy chain having at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 724, SEQ ID NO: 725, SEQ ID NO: 726, SEQ ID NO: 727, SEQ ID NO: 728, SEQ ID NO: 729, SEQ ID NO: 730, SEQ ID NO: 731, SEQ ID NO: 732, SEQ ID NO: 733, SEQ ID NO: 734, SEQ ID NO: 735, SEQ ID NO: 736, SEQ ID NO: 737, SEQ ID NO: 738, SEQ ID NO: 739, SEQ ID NO: 740, SEQ ID NO: 741, SEQ ID NO: 742, SEQ ID NO: 743, SEQ ID NO: 744, SEQ ID NO: 745, SEQ ID NO: 746, SEQ ID NO: 747, SEQ ID NO: 748, SEQ ID NO: 749, SEQ ID NO: 750, SEQ ID NO: 751,

IgG1 isotype. In specific embodiments, the cysteine in the Cys-Asp-Lys-Thr-His-Thr-X (CDKTHTX) sequence at the C' Terminal end is attached to a polymer (e.g., a PEG polymer). In specific embodiments, when X is C, the two cysteines in the Cys-Asp-Lys-Thr-His-Thr-X (CDKTHTX) sequence at the C' Terminal end are each attached to a polymer (e.g., a PEG polymer). In specific embodiments, when X is C, the second cysteine in the Cys-Asp-Lys-Thr-His-Thr-X (CDKTHTX) sequence at the C' Terminal end is attached to a polymer (e.g., a PEG polymer).

Table 8. Heavy chain and light chain amino acid sequences of C' terminal-modified anti-Factor D antibodies

10	SEQ ID NO: 180	C' terminal-modified AFD WT Heavy Chain	EVQLVQSGPELKKPGASVKVSCASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCERE GGVNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCD
15	SEQ ID NO: 181	C' terminal-modified AFD.v1 Heavy Chain	EVQLVQSGPELKKPGASVKVSCASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCERE GGVNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCD
20	SEQ ID NO: 182	C' terminal-modified AFD.v2 Heavy Chain	EVQLVQSGPELKKPGASVKVSCASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCERE GGVNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCD
25	SEQ ID NO: 183	C' terminal-modified AFD.v3 Heavy Chain	EVQLVQSGPELKKPGASVKVSCASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCERE GGVNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCD
30	SEQ ID NO: 184	C' terminal-modified AFD.v4 Heavy Chain	EVQLVQSGPELKKPGASVKVSCASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCERE GGVNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCD
35	SEQ ID NO: 185	C' terminal-modified AFD.v5 Heavy Chain	EVQLVQSGPELKKPGASVKVSCASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCERE GGVNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCD
40	SEQ ID NO: 186	C' terminal-modified AFD.v6 Heavy Chain	EVQLVQSGPELKKPGASVKVSCASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCERE GGVNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCD
45	SEQ ID NO: 187	C' terminal-modified AFD.v7 Heavy Chain	EVQLVQSGPELKKPGASVKVSCASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCERE GGVNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCD
50	SEQ ID NO: 188	C' terminal-modified AFD.v8 Heavy Chain	EVQLVQSGPELKKPGASVKVSCASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCERE GGVNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCD

(continued)

5	SEQ ID NO: 189	C' terminal-modified AFD.v9 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGLG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCD
10	SEQ ID NO: 190	C' terminal-modified AFD.v10 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGLG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCD
15	SEQ ID NO: 191	C' terminal-modified AFD.v11 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WISTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGLG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCD
20	SEQ ID NO: 192	C' terminal-modified AFD.v12 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGLG VDNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCD
25	SEQ ID NO: 193	C' terminal-modified AFD.v13 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGLG VQNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCD
30	SEQ ID NO: 194	C' terminal-modified AFD.v14 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGLG VSNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCD
35	SEQ ID NO: 195	C' terminal-modified AFD.v15 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGLG VSNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCD
40	SEQ ID NO: 196	C' terminal-modified huAFD.v2.0 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFKNEFKSRATLTVDSTSTAYLELSSLRSEDVAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCD
45	SEQ ID NO: 197	C' terminal-modified huAFD.v2.1 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFKNEFKSRATLTVDSTSTAYLELSSLRSEDVAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCD
50	SEQ ID NO: 198	C' terminal-modified huAFD.v2.3 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPYSGDTNFKNEFKSRATLTVDSTSTAYLELSSLRSEDVAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCD

(continued)

5	SEQ ID NO: 199	C' terminal-modified huAFD.v1 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTNGGTNFNEKFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGF AYWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSCD
10	SEQ ID NO: 200	C' terminal-modified huAFD.v1.1 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTQGGTNFNEKFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGF AYWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSCD
15	SEQ ID NO: 201	C' terminal-modified huAFD.v2.2 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGDTNFNEKFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCD
20	SEQ ID NO: 202	C' terminal-modified huAFD.v2.4 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGETNFNEKFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCD
25	SEQ ID NO: 203	C' terminal-modified huAFD.v2.5 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPYSGGTNFNEKFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCD
30	SEQ ID NO: 204	C' terminal-modified huAFD.v2.6 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCD
35	SEQ ID NO: 205	C' terminal-modified huAFD.v2.7 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCD
40	SEQ ID NO: 206	C' terminal-modified huAFD.v2.8 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCD
45	SEQ ID NO: 207	C' terminal-modified huAFD.v2.9 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIG WINPTSGGTNFNEKFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGG FAYWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCD
50	SEQ ID NO: 208	C' terminal-modified huAFD.v2.10 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCD

(continued)

5	SEQ ID NO: 209	C' terminal- modified huAFD.v2.11 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFKNEKFKSRATLTVDLTSTSTAYLELSSLRSEDVAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCD
10	SEQ ID NO: 210	C' terminal- modified huAFD.v2.12 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPYSGGTNFKNEKFKSRATLTVDLTSTSTAYLELSSLRSEDVAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCD
15	SEQ ID NO: 211	C' terminal- modified huAFD.v2.13 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFKNEKFKSRATLTVDLTSTSTAYLELSSLRSEDVAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCD
20	SEQ ID NO: 212	C' terminal- modified huAFD.v2.14 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFKNEKFKSRATLTVDLTSTSTAYLELSSLRSEDVAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCD
25	SEQ ID NO: 213	C' terminal- modified huAFD.v2.15 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPYSGGTNFKNEKFKSRATLTVDLTSTSTAYLELSSLRSEDVAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCD
30	SEQ ID NO: 214	C' terminal- modified AFD WT Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREKG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHL
35	SEQ ID NO: 215	C' terminal- modified AFD.v1 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREKG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHL
40	SEQ ID NO: 216	C' terminal- modified AFD.v2 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREKG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHL
45	SEQ ID NO: 217	C' terminal- modified AFD.v3 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREKG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHL
50	SEQ ID NO: 218	C' terminal- modified AFD.v4 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREKG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHL

(continued)

5	SEQ ID NO: 219	C' terminal- modified AFD.v5 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWRQAPGGGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHL
10	SEQ ID NO: 220	C' terminal- modified AFD.v6 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWRQAPGGGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHL
15	SEQ ID NO: 221	C' terminal- modified AFD.v7 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWRQAPGGGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHL
20	SEQ ID NO: 222	C' terminal- modified AFD.v8 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWRQAPGGGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHL
25	SEQ ID NO: 223	C' terminal- modified AFD.v9 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWRQAPGGGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHL
30	SEQ ID NO: 224	C' terminal- modified AFD.v10 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWRQAPGGGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHL
35	SEQ ID NO: 225	C' terminal- modified AFD.v1 1 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWRQAPGGGLEWMG WISTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHL
40	SEQ ID NO: 226	C' terminal- modified AFD.v12 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWRQAPGGGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VDNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHL
45	SEQ ID NO: 227	C' terminal- modified AFD.v13 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWRQAPGGGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VQNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHL
50	SEQ ID NO: 228	C' terminal- modified AFD.v14 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWRQAPGGGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VSNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHL

(continued)

5	SEQ ID NO: 229	C' terminal-modified AFD.v15 Heavy Chain	EVQLVQSGPELKKPGASVKV SCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCERE GG VSNWGQGT LVT VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHL
10	SEQ ID NO: 230	C' terminal-modified huAFD.v2.0 Heavy Chain	EVQLVQSGAEVKKPGASVKV SCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKF KSRATLTVD TSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGT LVT VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHL
15	SEQ ID NO: 231	C' terminal-modified huAFD.v2.1 Heavy Chain	EVQLVQSGAEVKKPGASVKV SCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKF KSRATLTVD TSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGT LVT VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHL
20	SEQ ID NO: 232	C' terminal-modified huAFD.v2.3 Heavy Chain	EVQLVQSGAEVKKPGASVKV SCKASGYTFTSYMYWVRQAPGQGLEWIGE INPYSGDTNFNEKF KSRATLTVD TSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGT LVT VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHL
25	SEQ ID NO: 233	C' terminal-modified huAFD.v1 Heavy Chain	EVQLVQSGAEVKKPGASVKV SCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTNGGTNFNEKF KSRATLTVD TSTSTAYLELSSLRSEDTAVYYCAREGGF AYWGQGT LVT VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSCDKTHL
30	SEQ ID NO: 234	C' terminal-modified huAFD.v1.1 Heavy Chain	EVQLVQSGAEVKKPGASVKV SCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTQGGTNFNEKF KSRATLTVD TSTSTAYLELSSLRSEDTAVYYCAREGGF AYWGQGT LVT VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSCDKTHL
35	SEQ ID NO: 235	C' terminal-modified huAFD.v2.2 Heavy Chain	EVQLVQSGAEVKKPGASVKV SCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGDTNFNEKF KSRATLTVD TSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGT LVT VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHL
40	SEQ ID NO: 236	C' terminal-modified huAFD.v2.4 Heavy Chain	EVQLVQSGAEVKKPGASVKV SCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGETNFNEKF KSRATLTVD TSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGT LVT VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHL
45	SEQ ID NO: 237	C' terminal-modified huAFD.v2.5 Heavy Chain	EVQLVQSGAEVKKPGASVKV SCKASGYTFTSYMYWVRQAPGQGLEWIGE INPYSGGTNFNEKF KSRATLTVD TSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGT LVT VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHL
50	SEQ ID NO: 238	C' terminal-modified huAFD.v2.6 Heavy Chain	EVQLVQSGAEVKKPGASVKV SCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKF KSRATLTVD TSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGT LVT VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHL

(continued)

5	SEQ ID NO: 239	C' terminal-modified huAFD.v2.7 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDLTSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHL
10	SEQ ID NO: 240	C' terminal-modified huAFD.v2.8 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDLTSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHL
15	SEQ ID NO: 241	C' terminal-modified huAFD.v2.9 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIG WINPTSGGTNFNEKFKSRATLTVDLTSTSTAYLELSSLRSEDTAVYYCAREGG FAYWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHL
20	SEQ ID NO: 242	C' terminal-modified huAFD.v2.10 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDLTSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHL
25	SEQ ID NO: 243	C' terminal-modified huAFD.v2.11 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDLTSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHL
30	SEQ ID NO: 244	C' terminal-modified huAFD.v2.12 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPYSGGTNFNEKFKSRATLTVDLTSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHL
35	SEQ ID NO: 245	C' terminal-modified huAFD.v2.13 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDLTSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHL
40	SEQ ID NO: 246	C' terminal-modified huAFD.v2.14 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDLTSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHL
45	SEQ ID NO: 247	C' terminal-modified huAFD.v2.15 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPYSGGTNFNEKFKSRATLTVDLTSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHL
50	SEQ ID NO: 248	C' terminal-modified AFD WT Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCAREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDK

(continued)

5	SEQ ID NO: 249	C' terminal-modified AFD.v1 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDK
10	SEQ ID NO: 250	C' terminal-modified AFD.v2 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDK
15	SEQ ID NO: 251	C' terminal-modified AFD.v3 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDK
20	SEQ ID NO: 252	C' terminal-modified AFD.v4 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDK
25	SEQ ID NO: 253	C' terminal-modified AFD.v5 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDK
30	SEQ ID NO: 254	C' terminal-modified AFD.v6 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDK
35	SEQ ID NO: 255	C' terminal-modified AFD.v7 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDK
40	SEQ ID NO: 256	C' terminal-modified AFD.v8 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDK
45	SEQ ID NO: 257	C' terminal-modified AFD.v9 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDK
50	SEQ ID NO: 258	C' terminal-modified AFD.v10 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDK

(continued)

5	SEQ ID NO: 259	C' terminal-modified AFD.v1 1 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WISTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCERE GG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDK
10	SEQ ID NO: 260	C' terminal-modified AFD.v12 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCERE GG VDNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDK
15	SEQ ID NO: 261	C' terminal-modified AFD.v13 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCERE GG VQNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDK
20	SEQ ID NO: 262	C' terminal-modified AFD.v14 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCERE GG VSNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDK
25	SEQ ID NO: 263	C' terminal-modified AFD.v15 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCERE GG VSNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDK
30	SEQ ID NO: 264	C' terminal-modified huAFD.v2.0 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFKNEFKSRATLTVDSTSTAYLELSSLRSED TAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDK
35	SEQ ID NO: 265	C' terminal-modified huAFD.v2.1 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFKNEFKSRATLTVDSTSTAYLELSSLRSED TAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDK
40	SEQ ID NO: 266	C' terminal-modified huAFD.v2.3 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPYS GDTNFKNEFKSRATLTVDSTSTAYLELSSLRSED TAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDK
45	SEQ ID NO: 267	C' terminal-modified huAFD.v1 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTNGGTNFKNEFKSRATLTVDSTSTAYLELSSLRSED TAVYYCAREGGF AYWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSCDK
50	SEQ ID NO: 268	C' terminal-modified huAFD.v1.1 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTQGGTNFKNEFKSRATLTVDSTSTAYLELSSLRSED TAVYYCAREGGF AYWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSCDK

(continued)

5	SEQ ID NO: 269	C' terminal- modified huAFD.v2.2 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGDTNFNEKFKSRATLTVDSTSTAYLELSSLRSEDNAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDK
10	SEQ ID NO: 270	C' terminal- modified huAFD.v2.4 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGETNFNEKFKSRATLTVDSTSTAYLELSSLRSEDNAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDK
15	SEQ ID NO: 271	C' terminal- modified huAFD.v2.5 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPYSGGTNFNEKFKSRATLTVDSTSTAYLELSSLRSEDNAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDK
20	SEQ ID NO: 272	C' terminal- modified huAFD.v2.6 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDSTSTAYLELSSLRSEDNAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDK
25	SEQ ID NO: 273	C' terminal- modified huAFD.v2.7 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDSTSTAYLELSSLRSEDNAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDK
30	SEQ ID NO: 274	C' terminal- modified huAFD.v2.8 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDSTSTAYLELSSLRSEDNAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDK
35	SEQ ID NO: 275	C' terminal- modified huAFD.v2.9 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIG WINPTSGGTNFNEKFKSRATLTVDSTSTAYLELSSLRSEDNAVYYCAREGG FAYWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDK
40	SEQ ID NO: 276	C' terminal- modified huAFD.v2.10 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDSTSTAYLELSSLRSEDNAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDK
45	SEQ ID NO: 277	C' terminal- modified huAFD.v2.11 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDSTSTAYLELSSLRSEDNAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDK
50	SEQ ID NO: 278	C' terminal- modified huAFD.v2.12 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPYSGGTNFNEKFKSRATLTVDSTSTAYLELSSLRSEDNAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDK

(continued)

5	SEQ ID NO: 279	C' terminal-modified huAFD.v2.13 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDSTSTAYLELSSLRSEDVAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDK
10	SEQ ID NO: 280	C' terminal-modified huAFD.v2.14 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDSTSTAYLELSSLRSEDVAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDK
15	SEQ ID NO: 281	C' terminal-modified huAFD.v2.15 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDSTSTAYLELSSLRSEDVAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDK
20	SEQ ID NO: 282	C' terminal-modified AFD WT Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREKG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKT
25	SEQ ID NO: 283	C' terminal-modified AFD.v1 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREKG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKT
30	SEQ ID NO: 284	C' terminal-modified AFD.v2 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREKG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKT
35	SEQ ID NO: 285	C' terminal-modified AFD.v3 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREKG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKT
40	SEQ ID NO: 286	C' terminal-modified AFD.v4 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREKG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKT
45	SEQ ID NO: 287	C' terminal-modified AFD.v5 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREKG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKT
50	SEQ ID NO: 288	C' terminal-modified AFD.v6 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREKG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKT

(continued)

5	SEQ ID NO: 289	C' terminal- modified AFD.v7 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGL VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKT
10	SEQ ID NO: 290	C' terminal- modified AFD.v8 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGL VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKT
15	SEQ ID NO: 291	C' terminal- modified AFD.v9 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGL VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKT
20	SEQ ID NO: 292	C' terminal- modified AFD.v10 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGL VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKT
25	SEQ ID NO: 293	C' terminal- modified AFD.v1 1 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWRQAPGQGLEWMG WISTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGL VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKT
30	SEQ ID NO: 294	C' terminal- modified AFD.v12 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGL VDNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKT
35	SEQ ID NO: 295	C' terminal- modified AFD.v13 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGL VQNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKT
40	SEQ ID NO: 296	C' terminal- modified AFD.v14 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGL VSNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKT
45	SEQ ID NO: 297	C' terminal- modified AFD.v15 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGL VSNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKT
50	SEQ ID NO: 298	C' terminal- modified huAFD.v2.0 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFEKFKSRATLTVDSTSTAYLELSSLRSED TAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKT

(continued)

5	SEQ ID NO: 299	C' terminal- modified huAFD.v2.1 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDSTSTAYLELSSLRSEDNAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKT
10	SEQ ID NO: 300	C' terminal- modified huAFD.v2.3 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPYSGDTNFNEKFKSRATLTVDSTSTAYLELSSLRSEDNAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKT
15	SEQ ID NO: 301	C' terminal- modified huAFD.v1 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTNGGTNFNEKFKSRATLTVDSTSTAYLELSSLRSEDNAVYYCAREGGF AYWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSCDKT
20	SEQ ID NO: 302	C' terminal- modified huAFD.v1.1 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTQGGTNFNEKFKSRATLTVDSTSTAYLELSSLRSEDNAVYYCAREGGF AYWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSCDKT
25	SEQ ID NO: 303	C' terminal- modified huAFD.v2.2 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGDTNFNEKFKSRATLTVDSTSTAYLELSSLRSEDNAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKT
30	SEQ ID NO: 304	C' terminal- modified huAFD.v2.4 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGETNFNEKFKSRATLTVDSTSTAYLELSSLRSEDNAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKT
35	SEQ ID NO: 305	C' terminal- modified huAFD.v2.5 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPYSGGTNFNEKFKSRATLTVDSTSTAYLELSSLRSEDNAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKT
40	SEQ ID NO: 306	C' terminal- modified huAFD.v2.6 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDSTSTAYLELSSLRSEDNAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKT
45	SEQ ID NO: 307	C' terminal- modified huAFD.v2.7 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDSTSTAYLELSSLRSEDNAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKT
50	SEQ ID NO: 308	C' terminal- modified huAFD.v2.8 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDSTSTAYLELSSLRSEDNAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKT

(continued)

5	SEQ ID NO: 309	C' terminal-modified huAFD.v2.9 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIG WINPTSGGTNFNEKFKSRATLTVDLTSTSTAYLELSSLRSEDVAVYYCAREGG FAYWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKT
10	SEQ ID NO: 310	C' terminal-modified huAFD.v2.10 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDLTSTSTAYLELSSLRSEDVAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKT
15	SEQ ID NO: 311	C' terminal-modified huAFD.v2.11 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDLTSTSTAYLELSSLRSEDVAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKT
20	SEQ ID NO: 312	C' terminal-modified huAFD.v2.12 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPYSGGTNFNEKFKSRATLTVDLTSTSTAYLELSSLRSEDVAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKT
25	SEQ ID NO: 313	C' terminal-modified huAFD.v2.13 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDLTSTSTAYLELSSLRSEDVAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKT
30	SEQ ID NO: 314	C' terminal-modified huAFD.v2.14 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDLTSTSTAYLELSSLRSEDVAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKT
35	SEQ ID NO: 315	C' terminal-modified huAFD.v2.15 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPYSGETNFNEKFKSRATLTVDLTSTSTAYLELSSLRSEDVAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKT
40	SEQ ID NO: 316	C' terminal-modified AFD WT Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREKG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTH
45	SEQ ID NO: 317	C' terminal-modified AFD.v1 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREKG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTH
50	SEQ ID NO: 318	C' terminal-modified AFD.v2 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREKG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTH
55			

(continued)

5	SEQ ID NO: 319	C' terminal-modified AFD.v3 Heavy Chain	EVQLVQSGPELKKPGASVKV SCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFV FSLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGT LTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSV VTPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTH
10	SEQ ID NO: 320	C' terminal-modified AFD.v4 Heavy Chain	EVQLVQSGPELKKPGASVKV SCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFV FSLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGT LTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSV VTPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTH
15	SEQ ID NO: 321	C' terminal-modified AFD.v5 Heavy Chain	EVQLVQSGPELKKPGASVKV SCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFV FSLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGT LTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSV VTPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTH
20	SEQ ID NO: 322	C' terminal-modified AFD.v6 Heavy Chain	EVQLVQSGPELKKPGASVKV SCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFV FSLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGT LTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSV VTPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTH
25	SEQ ID NO: 323	C' terminal-modified AFD.v7 Heavy Chain	EVQLVQSGPELKKPGASVKV SCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFV FSLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGT LTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSV VTPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTH
30	SEQ ID NO: 324	C' terminal-modified AFD.v8 Heavy Chain	EVQLVQSGPELKKPGASVKV SCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFV FSLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGT LTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSV VTPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTH
35	SEQ ID NO: 325	C' terminal-modified AFD.v9 Heavy Chain	EVQLVQSGPELKKPGASVKV SCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFV FSLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGT LTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSV VTPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTH
40	SEQ ID NO: 326	C' terminal-modified AFD.v10 Heavy Chain	EVQLVQSGPELKKPGASVKV SCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFV FSLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGT LTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSV VTPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTH
45	SEQ ID NO: 327	C' terminal-modified AFD.v11 Heavy Chain	EVQLVQSGPELKKPGASVKV SCKASGYTFTNYGMNWVRQAPGQGLEWMG WISTYTGETTYAEDFKGRFV FSLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGT LTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSV VTPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTH
50	SEQ ID NO: 328	C' terminal-modified AFD.v12 Heavy Chain	EVQLVQSGPELKKPGASVKV SCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFV FSLDTSVSTAYLQISSLKAEDTAVYYCEREGG VDNWGQGT LTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSV VTPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTH

(continued)

5	SEQ ID NO: 329	C' terminal-modified AFD.v13 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEEDTAVYYCEREGL VQNWGGTLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTH
10	SEQ ID NO: 330	C' terminal-modified AFD.v14 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEEDTAVYYCEREGL VSNWGGTLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTH
15	SEQ ID NO: 331	C' terminal-modified AFD.v15 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEEDTAVYYCEREGL VSNWGGTLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTH
20	SEQ ID NO: 332	C' terminal-modified huAFD.v2.0 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFKNEFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTH
25	SEQ ID NO: 333	C' terminal-modified huAFD.v2.1 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFKNEFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTH
30	SEQ ID NO: 334	C' terminal-modified huAFD.v2.3 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPYSGDTNFKNEFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTH
35	SEQ ID NO: 335	C' terminal-modified huAFD.v1 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTNGGTNFKNEFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGF AYWGQGTLLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSCDKTH
40	SEQ ID NO: 336	C' terminal-modified huAFD.v1.1 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTQGGTNFKNEFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGF AYWGQGTLLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSCDKTH
45	SEQ ID NO: 337	C' terminal-modified huAFD.v2.2 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGDTNFKNEFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTH
50	SEQ ID NO: 338	C' terminal-modified huAFD.v2.4 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGDTNFKNEFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTH

(continued)

5	SEQ ID NO: 339	C' terminal-modified huAFD.v2.5 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPYSGGTNFKNEKFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTH
10	SEQ ID NO: 340	C' terminal-modified huAFD.v2.6 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFKNEKFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTH
15	SEQ ID NO: 341	C' terminal-modified huAFD.v2.7 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFKNEKFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTH
20	SEQ ID NO: 342	C' terminal-modified huAFD.v2.8 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFKNEKFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTH
25	SEQ ID NO: 343	C' terminal-modified huAFD.v2.9 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIG WINPTSGGTNFKNEKFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGG FAYWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTH
30	SEQ ID NO: 344	C' terminal-modified huAFD.v2.10 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFKNEKFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTH
35	SEQ ID NO: 345	C' terminal-modified huAFD.v2.11 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFKNEKFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTH
40	SEQ ID NO: 346	C' terminal-modified huAFD.v2.12 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPYSGGTNFKNEKFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTH
45	SEQ ID NO: 347	C' terminal-modified huAFD.v2.13 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFKNEKFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTH
50	SEQ ID NO: 348	C' terminal-modified huAFD.v2.14 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFKNEKFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTH

(continued)

5	SEQ ID NO: 349	C' terminal-modified huAFD.v2.15 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPYSGETNFNEKFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTH
10	SEQ ID NO: 350	C' terminal-modified AFD WT Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTC
15	SEQ ID NO: 351	C' terminal-modified AFD.v1 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTC
20	SEQ ID NO: 352	C' terminal-modified AFD.v2 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTC
25	SEQ ID NO: 353	C' terminal-modified AFD.v3 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTC
30	SEQ ID NO: 354	C' terminal-modified AFD.v4 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTC
35	SEQ ID NO: 355	C' terminal-modified AFD.v5 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTC
40	SEQ ID NO: 356	C' terminal-modified AFD.v6 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTC
45	SEQ ID NO: 357	C' terminal-modified AFD.v7 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTC
50	SEQ ID NO: 358	C' terminal-modified AFD.v8 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTC

(continued)

5	SEQ ID NO: 359	C' terminal-modified AFD.v9 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEADVYYCEREGL VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTC
10	SEQ ID NO: 360	C' terminal-modified AFD.v10 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEADVYYCEREGL VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTC
15	SEQ ID NO: 361	C' terminal-modified AFD.v11 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWRQAPGQGLEWMG WISTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEADVYYCEREGL VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTC
20	SEQ ID NO: 362	C' terminal-modified AFD.v12 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEADVYYCEREGL VDNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTC
25	SEQ ID NO: 363	C' terminal-modified AFD.v13 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEADVYYCEREGL VQNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTC
30	SEQ ID NO: 364	C' terminal-modified AFD.v14 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEADVYYCEREGL VSNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTC
35	SEQ ID NO: 365	C' terminal-modified AFD.v15 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEADVYYCEREGL VSNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTC
40	SEQ ID NO: 366	C' terminal-modified huAFD.v2.0 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFKNEFKSRATLTVDSTSTAYLELSSLRSEDADVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTC
45	SEQ ID NO: 367	C' terminal-modified huAFD.v2.1 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFKNEFKSRATLTVDSTSTAYLELSSLRSEDADVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTC
50	SEQ ID NO: 368	C' terminal-modified huAFD.v2.3 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPYSGDTNFKNEFKSRATLTVDSTSTAYLELSSLRSEDADVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTC

(continued)

5	SEQ ID NO: 369	C' terminal-modified huAFD.v1 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTNGGTNFNEKFKSRATLTVDSTSTAYLELSSLRSEDVAVYYCAREGGF AYWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSCDKTHTC
10	SEQ ID NO: 370	C' terminal-modified huAFD.v1.1 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTQGGTNFNEKFKSRATLTVDSTSTAYLELSSLRSEDVAVYYCAREGGF AYWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSCDKTHTC
15	SEQ ID NO: 371	C' terminal-modified huAFD.v2.2 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGDTNFNEKFKSRATLTVDSTSTAYLELSSLRSEDVAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTC
20	SEQ ID NO: 372	C' terminal-modified huAFD.v2.4 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGETNFNEKFKSRATLTVDSTSTAYLELSSLRSEDVAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTC
25	SEQ ID NO: 373	C' terminal-modified huAFD.v2.5 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPYSGGTNFNEKFKSRATLTVDSTSTAYLELSSLRSEDVAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTC
30	SEQ ID NO: 374	C' terminal-modified huAFD.v2.6 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDSTSTAYLELSSLRSEDVAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTC
35	SEQ ID NO: 375	C' terminal-modified huAFD.v2.7 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDSTSTAYLELSSLRSEDVAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTC
40	SEQ ID NO: 376	C' terminal-modified huAFD.v2.8 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDSTSTAYLELSSLRSEDVAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTC
45	SEQ ID NO: 377	C' terminal-modified huAFD.v2.9 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIG WINPTSGGTNFNEKFKSRATLTVDSTSTAYLELSSLRSEDVAVYYCAREGG FAYWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTC
50	SEQ ID NO: 378	C' terminal-modified huAFD.v2.10 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDSTSTAYLELSSLRSEDVAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTC

(continued)

5	SEQ ID NO: 379	C' terminal-modified huAFD.v2.11 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFKNEKFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTC
10	SEQ ID NO: 380	C' terminal-modified huAFD.v2.12 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPYSGGTNFKNEKFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTC
15	SEQ ID NO: 381	C' terminal-modified huAFD.v2.13 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFKNEKFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTC
20	SEQ ID NO: 382	C' terminal-modified huAFD.v2.14 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFKNEKFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTC
25	SEQ ID NO: 383	C' terminal-modified huAFD.v2.15 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPYSGGTNFKNEKFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTC
30	SEQ ID NO: 384	C' terminal-modified AFD WT Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREKG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPC
35	SEQ ID NO: 385	C' terminal-modified AFD.v1 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREKG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPC
40	SEQ ID NO: 386	C' terminal-modified AFD.v2 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREKG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPC
45	SEQ ID NO: 387	C' terminal-modified AFD.v3 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREKG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPC
50	SEQ ID NO: 388	C' terminal-modified AFD.v4 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREKG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPC
55	SEQ ID NO: 388	C' terminal-modified AFD.v4 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREKG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPC

(continued)

5	SEQ ID NO: 389	C' terminal- modified AFD.v5 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPC
10	SEQ ID NO: 390	C' terminal- modified AFD.v6 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPC
15	SEQ ID NO: 391	C' terminal- modified AFD.v7 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPC
20	SEQ ID NO: 392	C' terminal- modified AFD.v8 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPC
25	SEQ ID NO: 393	C' terminal- modified AFD.v9 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPC
30	SEQ ID NO: 394	C' terminal- modified AFD.v10 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPC
35	SEQ ID NO: 395	C' terminal- modified AFD.v11 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWRQAPGQGLEWMG WISTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPC
40	SEQ ID NO: 396	C' terminal- modified AFD.v12 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VDNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPC
45	SEQ ID NO: 397	C' terminal- modified AFD.v13 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VQNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPC
50	SEQ ID NO: 398	C' terminal- modified AFD.v14 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VSNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPC

(continued)

5	SEQ ID NO: 399	C' terminal-modified AFD.v15 Heavy Chain	EVQLVQSGPELKKPGASVKVSKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREKG VSNWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPC
10	SEQ ID NO: 400	C' terminal-modified huAFD.v2.0 Heavy Chain	EVQLVQSGAEVKKPGASVKVSKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDSTSTAYLELSSLRSEDVAVYYCAREGGFA YWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTCPPC
15	SEQ ID NO: 401	C' terminal-modified huAFD.v2.1 Heavy Chain	EVQLVQSGAEVKKPGASVKVSKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDSTSTAYLELSSLRSEDVAVYYCAREGGFA YWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTCPPC
20	SEQ ID NO: 402	C' terminal-modified huAFD.v2.3 Heavy Chain	EVQLVQSGAEVKKPGASVKVSKASGYTFTSYMYWVRQAPGQGLEWIGE INPYSGDTNFNEKFKSRATLTVDSTSTAYLELSSLRSEDVAVYYCAREGGFA YWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTCPPC
25	SEQ ID NO: 403	C' terminal-modified huAFD.v1 Heavy Chain	EVQLVQSGAEVKKPGASVKVSKASGYTFTSYMYWVRQAPGQGLEWIGE INPTNGGTNFNEKFKSRATLTVDSTSTAYLELSSLRSEDVAVYYCAREGGF AYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSCDKTHTCPPC
30	SEQ ID NO: 404	C' terminal-modified huAFD.v1.1 Heavy Chain	EVQLVQSGAEVKKPGASVKVSKASGYTFTSYMYWVRQAPGQGLEWIGE INPTQGGTNFNEKFKSRATLTVDSTSTAYLELSSLRSEDVAVYYCAREGGF AYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSCDKTHTCPPC
35	SEQ ID NO: 405	C' terminal-modified huAFD.v2.2 Heavy Chain	EVQLVQSGAEVKKPGASVKVSKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGDTNFNEKFKSRATLTVDSTSTAYLELSSLRSEDVAVYYCAREGGFA YWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTCPPC
40	SEQ ID NO: 406	C' terminal-modified huAFD.v2.4 Heavy Chain	EVQLVQSGAEVKKPGASVKVSKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGETNFNEKFKSRATLTVDSTSTAYLELSSLRSEDVAVYYCAREGGFA YWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTCPPC
45	SEQ ID NO: 407	C' terminal-modified huAFD.v2.5 Heavy Chain	EVQLVQSGAEVKKPGASVKVSKASGYTFTSYMYWVRQAPGQGLEWIGE INPYSGGTNFNEKFKSRATLTVDSTSTAYLELSSLRSEDVAVYYCAREGGFA YWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTCPPC
50	SEQ ID NO: 408	C' terminal-modified huAFD.v2.6 Heavy Chain	EVQLVQSGAEVKKPGASVKVSKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDSTSTAYLELSSLRSEDVAVYYCAREGGFA YWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTCPPC

(continued)

5	SEQ ID NO: 409	C' terminal-modified huAFD.v2.7 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTCPPC
10	SEQ ID NO: 410	C' terminal-modified huAFD.v2.8 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTCPPC
15	SEQ ID NO: 411	C' terminal-modified huAFD.v2.9 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIG WINPTSGGTNFNEKFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGG FAYWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPC
20	SEQ ID NO: 412	C' terminal-modified huAFD.v2.10 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTCPPC
25	SEQ ID NO: 413	C' terminal-modified huAFD.v2.11 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTCPPC
30	SEQ ID NO: 414	C' terminal-modified huAFD.v2.12 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPYSGGTNFNEKFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTCPPC
35	SEQ ID NO: 415	C' terminal-modified huAFD.v2.13 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTCPPC
40	SEQ ID NO: 416	C' terminal-modified huAFD.v2.14 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTCPPC
45	SEQ ID NO: 417	C' terminal-modified huAFD.v2.15 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPYSGGTNFNEKFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTCPPC
50	SEQ ID NO: 418	C' terminal-modified AFD WT Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCAREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPS

(continued)

5	SEQ ID NO: 419	C' terminal-modified AFD.v1 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPS
10	SEQ ID NO: 420	C' terminal-modified AFD.v2 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPS
15	SEQ ID NO: 421	C' terminal-modified AFD.v3 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPS
20	SEQ ID NO: 422	C' terminal-modified AFD.v4 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPS
25	SEQ ID NO: 423	C' terminal-modified AFD.v5 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPS
30	SEQ ID NO: 424	C' terminal-modified AFD.v6 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPS
35	SEQ ID NO: 425	C' terminal-modified AFD.v7 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPS
40	SEQ ID NO: 426	C' terminal-modified AFD.v8 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPS
45	SEQ ID NO: 427	C' terminal-modified AFD.v9 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPS
50	SEQ ID NO: 428	C' terminal-modified AFD.v10 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPS

(continued)

5	SEQ ID NO: 429	C' terminal-modified AFD.v11 Heavy Chain	EVQLVQSGPELKKPGASVKVSCASGYTFTNYGMNWVRQAPGQGLEWMG WISTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCERE GG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPS
10	SEQ ID NO: 430	C' terminal-modified AFD.v12 Heavy Chain	EVQLVQSGPELKKPGASVKVSCASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCERE GG VDNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPS
15	SEQ ID NO: 431	C' terminal-modified AFD.v13 Heavy Chain	EVQLVQSGPELKKPGASVKVSCASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCERE GG VQNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPS
20	SEQ ID NO: 432	C' terminal-modified AFD.v14 Heavy Chain	EVQLVQSGPELKKPGASVKVSCASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCERE GG VSNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPS
25	SEQ ID NO: 433	C' terminal-modified AFD.v15 Heavy Chain	EVQLVQSGPELKKPGASVKVSCASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCERE GG VSNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPS
30	SEQ ID NO: 434	C' terminal-modified huAFD.v2.0 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFKNEFKSRATLTVDSTSTAYLELSSLRSED TAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTCPPS
35	SEQ ID NO: 435	C' terminal-modified huAFD.v2.1 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFKNEFKSRATLTVDSTSTAYLELSSLRSED TAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTCPPS
40	SEQ ID NO: 436	C' terminal-modified huAFD.v2.3 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCASGYTFTSYMYWVRQAPGQGLEWIGE INPYSGDTNFKNEFKSRATLTVDSTSTAYLELSSLRSED TAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTCPPS
45	SEQ ID NO: 437	C' terminal-modified huAFD.v1 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCASGYTFTSYMYWVRQAPGQGLEWIGE INPTNGGTNFKNEFKSRATLTVDSTSTAYLELSSLRSED TAVYYCAREGGF AYWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSCDKTHTCPPS
50	SEQ ID NO: 438	C' terminal-modified huAFD.v1.1 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCASGYTFTSYMYWVRQAPGQGLEWIGE INPTQGGTNFKNEFKSRATLTVDSTSTAYLELSSLRSED TAVYYCAREGGF AYWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSCDKTHTCPPS

(continued)

5	SEQ ID NO: 439	C' terminal- modified huAFD.v2.2 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGDTNFNEKFKSRATLTVDLTSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTCPPS
10	SEQ ID NO: 440	C' terminal- modified huAFD.v2.4 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGETNFNEKFKSRATLTVDLTSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTCPPS
15	SEQ ID NO: 441	C' terminal- modified huAFD.v2.5 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPYSGGTNFNEKFKSRATLTVDLTSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTCPPS
20	SEQ ID NO: 442	C' terminal- modified huAFD.v2.6 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDLTSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTCPPS
25	SEQ ID NO: 443	C' terminal- modified huAFD.v2.7 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDLTSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTCPPS
30	SEQ ID NO: 444	C' terminal- modified huAFD.v2.8 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDLTSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTCPPS
35	SEQ ID NO: 445	C' terminal- modified huAFD.v2.9 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIG WINPTSGGTNFNEKFKSRATLTVDLTSTSTAYLELSSLRSEDTAVYYCAREGG FAYWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPS
40	SEQ ID NO: 446	C' terminal- modified huAFD.v2.10 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDLTSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTCPPS
45	SEQ ID NO: 447	C' terminal- modified huAFD.v2.11 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDLTSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTCPPS
50	SEQ ID NO: 448	C' terminal- modified huAFD.v2.12 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPYSGGTNFNEKFKSRATLTVDLTSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTCPPS

(continued)

5	SEQ ID NO: 449	C' terminal- modified huAFD.v2.13 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDSTSTAYLELSSLRSEDNAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTCPPS
10	SEQ ID NO: 450	C' terminal- modified huAFD.v2.14 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDSTSTAYLELSSLRSEDNAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTCPPS
15	SEQ ID NO: 451	C' terminal- modified huAFD.v2.15 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDSTSTAYLELSSLRSEDNAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTCPPS
20	SEQ ID NO: 452	C' terminal- modified AFD WT Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDNAVYYCERE GGVNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTSPPC
25	SEQ ID NO: 453	C' terminal- modified AFD.v1 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDNAVYYCERE GGVNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTSPPC
30	SEQ ID NO: 454	C' terminal- modified AFD.v2 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDNAVYYCERE GGVNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTSPPC
35	SEQ ID NO: 455	C' terminal- modified AFD.v3 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDNAVYYCERE GGVNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTSPPC
40	SEQ ID NO: 456	C' terminal- modified AFD.v4 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDNAVYYCERE GGVNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTSPPC
45	SEQ ID NO: 457	C' terminal- modified AFD.v5 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDNAVYYCERE GGVNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTSPPC
50	SEQ ID NO: 458	C' terminal- modified AFD.v6 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDNAVYYCERE GGVNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTSPPC

(continued)

5	SEQ ID NO: 459	C' terminal-modified AFD.v7 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTSPPC
10	SEQ ID NO: 460	C' terminal-modified AFD.v8 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTSPPC
15	SEQ ID NO: 461	C' terminal-modified AFD.v9 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTSPPC
20	SEQ ID NO: 462	C' terminal-modified AFD.v10 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTSPPC
25	SEQ ID NO: 463	C' terminal-modified AFD.v11 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WISTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTSPPC
30	SEQ ID NO: 464	C' terminal-modified AFD.v12 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VDNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTSPPC
35	SEQ ID NO: 465	C' terminal-modified AFD.v13 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VQNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTSPPC
40	SEQ ID NO: 466	C' terminal-modified AFD.v14 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VSNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTSPPC
45	SEQ ID NO: 467	C' terminal-modified AFD.v15 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VSNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTSPPC
50	SEQ ID NO: 468	C' terminal-modified huAFD.v2.0 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFKNEFKSRATLTVDSTSTAYLELSSLRSED TAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTSPPC

(continued)

5	SEQ ID NO: 469	C' terminal- modified huAFD.v2.1 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDSTSTAYLELSSLRSEDNAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTSPPC
10	SEQ ID NO: 470	C' terminal- modified huAFD.v2.3 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPYSGDTNFNEKFKSRATLTVDSTSTAYLELSSLRSEDNAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTSPPC
15	SEQ ID NO: 471	C' terminal- modified huAFD.v1 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTNGGTNFNEKFKSRATLTVDSTSTAYLELSSLRSEDNAVYYCAREGGF AYWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSCDKTHTSPPC
20	SEQ ID NO: 472	C' terminal- modified huAFD.v1.1 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTQGGTNFNEKFKSRATLTVDSTSTAYLELSSLRSEDNAVYYCAREGGF AYWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSCDKTHTSPPC
25	SEQ ID NO: 473	C' terminal- modified huAFD.v2.2 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGDTNFNEKFKSRATLTVDSTSTAYLELSSLRSEDNAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTSPPC
30	SEQ ID NO: 474	C' terminal- modified huAFD.v2.4 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGETNFNEKFKSRATLTVDSTSTAYLELSSLRSEDNAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTSPPC
35	SEQ ID NO: 475	C' terminal- modified huAFD.v2.5 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPYSGGTNFNEKFKSRATLTVDSTSTAYLELSSLRSEDNAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTSPPC
40	SEQ ID NO: 476	C' terminal- modified huAFD.v2.6 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDSTSTAYLELSSLRSEDNAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTSPPC
45	SEQ ID NO: 477	C' terminal- modified huAFD.v2.7 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDSTSTAYLELSSLRSEDNAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTSPPC
50	SEQ ID NO: 478	C' terminal- modified huAFD.v2.8 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDSTSTAYLELSSLRSEDNAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTSPPC

(continued)

5	SEQ ID NO: 479	C' terminal-modified huAFD.v2.9 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIG WINPTSGGTNFNEKFKSRATLTVDVTSTSTAYLELSSLRSEDVAVYYCAREGG FAYWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTSPPC
10	SEQ ID NO: 480	C' terminal-modified huAFD.v2.10 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDVTSTSTAYLELSSLRSEDVAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTSPPC
15	SEQ ID NO: 481	C' terminal-modified huAFD.v2.11 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDVTSTSTAYLELSSLRSEDVAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTSPPC
20	SEQ ID NO: 482	C' terminal-modified huAFD.v2.12 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPYSGGTNFNEKFKSRATLTVDVTSTSTAYLELSSLRSEDVAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTSPPC
25	SEQ ID NO: 483	C' terminal-modified huAFD.v2.13 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDVTSTSTAYLELSSLRSEDVAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTSPPC
30	SEQ ID NO: 484	C' terminal-modified huAFD.v2.14 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDVTSTSTAYLELSSLRSEDVAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTSPPC
35	SEQ ID NO: 485	C' terminal-modified huAFD.v2.15 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPYSGETNFNEKFKSRATLTVDVTSTSTAYLELSSLRSEDVAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTSPPC
40	SEQ ID NO: 486	C' terminal-modified AFD WT Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREKG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTAPPC
45	SEQ ID NO: 487	C' terminal-modified AFD.v1 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREKG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTAPPC
50	SEQ ID NO: 488	C' terminal-modified AFD.v2 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREKG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTAPPC
55			

(continued)

5	SEQ ID NO: 489	C' terminal- modified AFD.v3 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTAPPC
10	SEQ ID NO: 490	C' terminal- modified AFD.v4 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTAPPC
15	SEQ ID NO: 491	C' terminal- modified AFD.v5 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTAPPC
20	SEQ ID NO: 492	C' terminal- modified AFD.v6 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTAPPC
25	SEQ ID NO: 493	C' terminal- modified AFD.v7 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTAPPC
30	SEQ ID NO: 494	C' terminal- modified AFD.v8 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTAPPC
35	SEQ ID NO: 495	C' terminal- modified AFD.v9 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTAPPC
40	SEQ ID NO: 496	C' terminal- modified AFD.v10 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTAPPC
45	SEQ ID NO: 497	C' terminal- modified AFD.v11 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWRQAPGQGLEWMG WISTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTAPPC
50	SEQ ID NO: 498	C' terminal- modified AFD.v12 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VDNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTAPPC

(continued)

5	SEQ ID NO: 499	C' terminal-modified AFD.v13 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEEDTAVYYCEREGLG VQNWGGTLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPV VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTAPPCC
10	SEQ ID NO: 500	C' terminal-modified AFD.v14 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEEDTAVYYCEREGLG VSNWGGTLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPV VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTAPPCC
15	SEQ ID NO: 501	C' terminal-modified AFD.v15 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEEDTAVYYCEREGLG VSNWGGTLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPV VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTAPPCC
20	SEQ ID NO: 502	C' terminal-modified huAFD.v2.0 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFKNEFKSRATLTVDTSSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPV VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTAPPCC
25	SEQ ID NO: 503	C' terminal-modified huAFD.v2.1 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFKNEFKSRATLTVDTSSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPV VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTAPPCC
30	SEQ ID NO: 504	C' terminal-modified huAFD.v2.3 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPYSGDTNFKNEFKSRATLTVDTSSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPV VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTAPPCC
35	SEQ ID NO: 505	C' terminal-modified huAFD.v1 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTNGGTNFKNEFKSRATLTVDTSSTAYLELSSLRSEDTAVYYCAREGGF AYWGQGTLLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPV VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSCDKTHTAPPCC
40	SEQ ID NO: 506	C' terminal-modified huAFD.v1.1 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTQGGTNFKNEFKSRATLTVDTSSTAYLELSSLRSEDTAVYYCAREGGF AYWGQGTLLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPV VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSCDKTHTAPPCC
45	SEQ ID NO: 507	C' terminal-modified huAFD.v2.2 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGDTNFKNEFKSRATLTVDTSSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPV VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTAPPCC
50	SEQ ID NO: 508	C' terminal-modified huAFD.v2.4 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGDTNFKNEFKSRATLTVDTSSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPV VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTAPPCC

(continued)

5	SEQ ID NO: 509	C' terminal- modified huAFD.v2.5 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPYSGGTNFKNEFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTAPP
10	SEQ ID NO: 510	C' terminal- modified huAFD.v2.6 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFKNEFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTAPP
15	SEQ ID NO: 511	C' terminal- modified huAFD.v2.7 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFKNEFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTAPP
20	SEQ ID NO: 512	C' terminal- modified huAFD.v2.8 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFKNEFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTAPP
25	SEQ ID NO: 513	C' terminal- modified huAFD.v2.9 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIG WINPTSGGTNFKNEFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGG FAYWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTAPP
30	SEQ ID NO: 514	C' terminal- modified huAFD.v2.10 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFKNEFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTAPP
35	SEQ ID NO: 515	C' terminal- modified huAFD.v2.11 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFKNEFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTAPP
40	SEQ ID NO: 516	C' terminal- modified huAFD.v2.12 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPYSGGTNFKNEFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTAPP
45	SEQ ID NO: 517	C' terminal- modified huAFD.v2.13 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFKNEFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTAPP
50	SEQ ID NO: 518	C' terminal- modified huAFD.v2.14 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFKNEFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTAPP

(continued)

5	SEQ ID NO: 519	C' terminal-modified huAFD.v2.15 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPYSGETNFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTAPPC
10	SEQ ID NO: 520	C' terminal-modified AFD WT Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTSGGC
15	SEQ ID NO: 521	C' terminal-modified AFD.v1 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTSGGC
20	SEQ ID NO: 522	C' terminal-modified AFD.v2 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTSGGC
25	SEQ ID NO: 523	C' terminal-modified AFD.v3 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTSGGC
30	SEQ ID NO: 524	C' terminal-modified AFD.v4 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTSGGC
35	SEQ ID NO: 525	C' terminal-modified AFD.v5 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTSGGC
40	SEQ ID NO: 526	C' terminal-modified AFD.v6 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTSGGC
45	SEQ ID NO: 527	C' terminal-modified AFD.v7 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTSGGC
50	SEQ ID NO: 528	C' terminal-modified AFD.v8 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTSGGC

(continued)

5	SEQ ID NO: 529	C' terminal-modified AFD.v9 Heavy Chain	EVQLVQSGPELKKPGASVKVSCASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCERE GG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTSGGC
10	SEQ ID NO: 530	C' terminal-modified AFD.v10 Heavy Chain	EVQLVQSGPELKKPGASVKVSCASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCERE GG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTSGGC
15	SEQ ID NO: 531	C' terminal-modified AFD.v11 Heavy Chain	EVQLVQSGPELKKPGASVKVSCASGYTFTNYGMNWVRQAPGQGLEWMG WISTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCERE GG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTSGGC
20	SEQ ID NO: 532	C' terminal-modified AFD.v12 Heavy Chain	EVQLVQSGPELKKPGASVKVSCASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCERE GG VDNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTSGGC
25	SEQ ID NO: 533	C' terminal-modified AFD.v13 Heavy Chain	EVQLVQSGPELKKPGASVKVSCASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCERE GG VQNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTSGGC
30	SEQ ID NO: 534	C' terminal-modified AFD.v14 Heavy Chain	EVQLVQSGPELKKPGASVKVSCASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCERE GG VSNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTSGGC
35	SEQ ID NO: 535	C' terminal-modified AFD.v15 Heavy Chain	EVQLVQSGPELKKPGASVKVSCASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCERE GG VSNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTSGGC
40	SEQ ID NO: 536	C' terminal-modified huAFD.v2.0 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFKNEFKSRATLTVDSTSTAYLELSSLRSED TAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTSGGC
45	SEQ ID NO: 537	C' terminal-modified huAFD.v2.1 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFKNEFKSRATLTVDSTSTAYLELSSLRSED TAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTSGGC
50	SEQ ID NO: 538	C' terminal-modified huAFD.v2.3 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCASGYTFTSYMYWVRQAPGQGLEWIGE INPYSGDTNFKNEFKSRATLTVDSTSTAYLELSSLRSED TAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTSGGC

(continued)

5	SEQ ID NO: 539	C' terminal-modified huAFD.v1 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTNGGTNFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGF AYWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT SWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSCDKTHTSGGC
10	SEQ ID NO: 540	C' terminal-modified huAFD.v1.1 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTQGGTNFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGF AYWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT SWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSCDKTHTSGGC
15	SEQ ID NO: 541	C' terminal-modified huAFD.v2.2 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGDTNFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSCDKTHTSGGC
20	SEQ ID NO: 542	C' terminal-modified huAFD.v2.4 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSCDKTHTSGGC
25	SEQ ID NO: 543	C' terminal-modified huAFD.v2.5 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPYSGGTNFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSCDKTHTSGGC
30	SEQ ID NO: 544	C' terminal-modified huAFD.v2.6 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSCDKTHTSGGC
35	SEQ ID NO: 545	C' terminal-modified huAFD.v2.7 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSCDKTHTSGGC
40	SEQ ID NO: 546	C' terminal-modified huAFD.v2.8 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSCDKTHTSGGC
45	SEQ ID NO: 547	C' terminal-modified huAFD.v2.9 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIG WINPTSGGTNFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGG FAYWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTSGGC
50	SEQ ID NO: 548	C' terminal-modified huAFD.v2.10 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSCDKTHTSGGC

(continued)

5	SEQ ID NO: 549	C' terminal-modified huAFD.v2.11 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFKNEKFKSRATLTVDSTSTAYLELSSLRSEDVAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTSGGC
10	SEQ ID NO: 550	C' terminal-modified huAFD.v2.12 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPYSGGTNFKNEKFKSRATLTVDSTSTAYLELSSLRSEDVAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTSGGC
15	SEQ ID NO: 551	C' terminal-modified huAFD.v2.13 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFKNEKFKSRATLTVDSTSTAYLELSSLRSEDVAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTSGGC
20	SEQ ID NO: 552	C' terminal-modified huAFD.v2.14 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFKNEKFKSRATLTVDSTSTAYLELSSLRSEDVAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTSGGC
25	SEQ ID NO: 553	C' terminal-modified huAFD.v2.15 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPYSGGTNFKNEKFKSRATLTVDSTSTAYLELSSLRSEDVAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTSGGC
30	SEQ ID NO: 554	C' terminal-modified AFD WT Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREKG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCYGPCC
35	SEQ ID NO: 555	C' terminal-modified AFD.v1 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREKG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCYGPCC
40	SEQ ID NO: 556	C' terminal-modified AFD.v2 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREKG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCYGPCC
45	SEQ ID NO: 557	C' terminal-modified AFD.v3 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREKG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCYGPCC
50	SEQ ID NO: 558	C' terminal-modified AFD.v4 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREKG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCYGPCC

(continued)

5	SEQ ID NO: 559	C' terminal-modified AFD.v5 Heavy Chain	EVQLVQSGPELKKPGASVKV SCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFSLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGT LTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCYGP
10	SEQ ID NO: 560	C' terminal-modified AFD.v6 Heavy Chain	EVQLVQSGPELKKPGASVKV SCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFSLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGT LTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCYGP
15	SEQ ID NO: 561	C' terminal-modified AFD.v7 Heavy Chain	EVQLVQSGPELKKPGASVKV SCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFSLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGT LTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCYGP
20	SEQ ID NO: 562	C' terminal-modified AFD.v8 Heavy Chain	EVQLVQSGPELKKPGASVKV SCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFSLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGT LTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCYGP
25	SEQ ID NO: 563	C' terminal-modified AFD.v9 Heavy Chain	EVQLVQSGPELKKPGASVKV SCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFSLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGT LTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCYGP
30	SEQ ID NO: 564	C' terminal-modified AFD.v10 Heavy Chain	EVQLVQSGPELKKPGASVKV SCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFSLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGT LTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCYGP
35	SEQ ID NO: 565	C' terminal-modified AFD.v11 Heavy Chain	EVQLVQSGPELKKPGASVKV SCKASGYTFTNYGMNWVRQAPGQGLEWMG WISTYTGETTYAEDFKGRFVFSLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGT LTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCYGP
40	SEQ ID NO: 566	C' terminal-modified AFD.v12 Heavy Chain	EVQLVQSGPELKKPGASVKV SCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFSLDTSVSTAYLQISSLKAEDTAVYYCEREGG VDNWGQGT LTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCYGP
45	SEQ ID NO: 567	C' terminal-modified AFD.v13 Heavy Chain	EVQLVQSGPELKKPGASVKV SCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFSLDTSVSTAYLQISSLKAEDTAVYYCEREGG VQNWGQGT LTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCYGP
50	SEQ ID NO: 568	C' terminal-modified AFD.v14 Heavy Chain	EVQLVQSGPELKKPGASVKV SCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFSLDTSVSTAYLQISSLKAEDTAVYYCEREGG VSNWGQGT LTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCYGP

(continued)

5	SEQ ID NO: 569	C' terminal-modified AFD.v15 Heavy Chain	EVQLVQSGPELKKPGASVKVSKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCERE GG VSNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCYGP
10	SEQ ID NO: 570	C' terminal-modified huAFD.v2.0 Heavy Chain	EVQLVQSGAEVKKPGASVKVSKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDSTSTAYLELSSLRSED TAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCYGP
15	SEQ ID NO: 571	C' terminal-modified huAFD.v2.1 Heavy Chain	EVQLVQSGAEVKKPGASVKVSKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDSTSTAYLELSSLRSED TAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCYGP
20	SEQ ID NO: 572	C' terminal-modified huAFD.v2.3 Heavy Chain	EVQLVQSGAEVKKPGASVKVSKASGYTFTSYMYWVRQAPGQGLEWIGE INPYSGDTNFNEKFKSRATLTVDSTSTAYLELSSLRSED TAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCYGP
25	SEQ ID NO: 573	C' terminal-modified huAFD.v1 Heavy Chain	EVQLVQSGAEVKKPGASVKVSKASGYTFTSYMYWVRQAPGQGLEWIGE INPTNGGTNFNEKFKSRATLTVDSTSTAYLELSSLRSED TAVYYCAREGGF AYWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSCYGP
30	SEQ ID NO: 574	C' terminal-modified huAFD.v1.1 Heavy Chain	EVQLVQSGAEVKKPGASVKVSKASGYTFTSYMYWVRQAPGQGLEWIGE INPTQGGTNFNEKFKSRATLTVDSTSTAYLELSSLRSED TAVYYCAREGGF AYWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSCYGP
35	SEQ ID NO: 575	C' terminal-modified huAFD.v2.2 Heavy Chain	EVQLVQSGAEVKKPGASVKVSKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGDTNFNEKFKSRATLTVDSTSTAYLELSSLRSED TAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCYGP
40	SEQ ID NO: 576	C' terminal-modified huAFD.v2.4 Heavy Chain	EVQLVQSGAEVKKPGASVKVSKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGETNFNEKFKSRATLTVDSTSTAYLELSSLRSED TAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCYGP
45	SEQ ID NO: 577	C' terminal-modified huAFD.v2.5 Heavy Chain	EVQLVQSGAEVKKPGASVKVSKASGYTFTSYMYWVRQAPGQGLEWIGE INPYSGGTNFNEKFKSRATLTVDSTSTAYLELSSLRSED TAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCYGP
50	SEQ ID NO: 578	C' terminal-modified huAFD.v2.6 Heavy Chain	EVQLVQSGAEVKKPGASVKVSKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDSTSTAYLELSSLRSED TAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCYGP

(continued)

5	SEQ ID NO: 579	C' terminal-modified huAFD.v2.7 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDLTSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCYGP
10	SEQ ID NO: 580	C' terminal-modified huAFD.v2.8 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDLTSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCYGP
15	SEQ ID NO: 581	C' terminal-modified huAFD.v2.9 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIG WINPTSGGTNFNEKFKSRATLTVDLTSTSTAYLELSSLRSEDTAVYYCAREGG FAYWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCYGP
20	SEQ ID NO: 582	C' terminal-modified huAFD.v2.10 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDLTSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCYGP
25	SEQ ID NO: 583	C' terminal-modified huAFD.v2.11 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDLTSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCYGP
30	SEQ ID NO: 584	C' terminal-modified huAFD.v2.12 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPYSGGTNFNEKFKSRATLTVDLTSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCYGP
35	SEQ ID NO: 585	C' terminal-modified huAFD.v2.13 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDLTSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCYGP
40	SEQ ID NO: 586	C' terminal-modified huAFD.v2.14 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDLTSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCYGP
45	SEQ ID NO: 587	C' terminal-modified huAFD.v2.15 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPYSGETNFNEKFKSRATLTVDLTSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCYGP
50	SEQ ID NO: 588	C' terminal-modified AFD WT Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCERE GGVNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSVERK

(continued)

5	SEQ ID NO: 589	C' terminal- modified AFD.v1 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSVERK
10	SEQ ID NO: 590	C' terminal- modified AFD.v2 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSVERK
15	SEQ ID NO: 591	C' terminal- modified AFD.v3 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSVERK
20	SEQ ID NO: 592	C' terminal- modified AFD.v4 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSVERK
25	SEQ ID NO: 593	C' terminal- modified AFD.v5 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSVERK
30	SEQ ID NO: 594	C' terminal- modified AFD.v6 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSVERK
35	SEQ ID NO: 595	C' terminal- modified AFD.v7 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSVERK
40	SEQ ID NO: 596	C' terminal- modified AFD.v8 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSVERK
45	SEQ ID NO: 597	C' terminal- modified AFD.v9 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSVERK
50	SEQ ID NO: 598	C' terminal- modified AFD.v10 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSVERK

(continued)

5	SEQ ID NO: 599	C' terminal- modified AFD.v11 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WISTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDEAVYYCEREGL VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSVERK
10	SEQ ID NO: 600	C' terminal- modified AFD.v12 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDEAVYYCEREGL VDNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSVERK
15	SEQ ID NO: 601	C' terminal- modified AFD.v13 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDEAVYYCEREGL VQNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSVERK
20	SEQ ID NO: 602	C' terminal- modified AFD.v14 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDEAVYYCEREGL VSNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSVERK
25	SEQ ID NO: 603	C' terminal- modified AFD.v15 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDEAVYYCEREGL VSNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSVERK
30	SEQ ID NO: 604	C' terminal- modified huAFD.v2.0 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFKNEFKSRATLTVDTSSTAYLELSSLRSEDEAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSVERK
35	SEQ ID NO: 605	C' terminal- modified huAFD.v2.1 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFKNEFKSRATLTVDTSSTAYLELSSLRSEDEAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSVERK
40	SEQ ID NO: 606	C' terminal- modified huAFD.v2.3 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPYSGDTNFKNEFKSRATLTVDTSSTAYLELSSLRSEDEAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSVERK
45	SEQ ID NO: 607	C' terminal- modified huAFD.v1 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTNGGTNFKNEFKSRATLTVDTSSTAYLELSSLRSEDEAVYYCAREGGF AYWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSVERK
50	SEQ ID NO: 608	C' terminal- modified huAFD.v1.1 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTQGGTNFKNEFKSRATLTVDTSSTAYLELSSLRSEDEAVYYCAREGGF AYWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSVERK

(continued)

5	SEQ ID NO: 609	C' terminal- modified huAFD.v2.2 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGDTNFNEKFKSRATLTVDSTSTAYLELSSLRSEDNAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSVERK
10	SEQ ID NO: 610	C' terminal- modified huAFD.v2.4 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGETNFNEKFKSRATLTVDSTSTAYLELSSLRSEDNAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSVERK
15	SEQ ID NO: 611	C' terminal- modified huAFD.v2.5 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPSSGGTNFNEKFKSRATLTVDSTSTAYLELSSLRSEDNAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSVERK
20	SEQ ID NO: 612	C' terminal- modified huAFD.v2.6 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDSTSTAYLELSSLRSEDNAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSVERK
25	SEQ ID NO: 613	C' terminal- modified huAFD.v2.7 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDSTSTAYLELSSLRSEDNAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSVERK
30	SEQ ID NO: 614	C' terminal- modified huAFD.v2.8 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDSTSTAYLELSSLRSEDNAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSVERK
35	SEQ ID NO: 615	C' terminal- modified huAFD.v2.9 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIG WINPTSGGTNFNEKFKSRATLTVDSTSTAYLELSSLRSEDNAVYYCAREGG FAYWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSVERK
40	SEQ ID NO: 616	C' terminal- modified huAFD.v2.10 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDSTSTAYLELSSLRSEDNAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSVERK
45	SEQ ID NO: 617	C' terminal- modified huAFD.v2.11 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDSTSTAYLELSSLRSEDNAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSVERK
50	SEQ ID NO: 618	C' terminal- modified huAFD.v2.12 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPSSGGTNFNEKFKSRATLTVDSTSTAYLELSSLRSEDNAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSVERK

(continued)

5	SEQ ID NO: 619	C' terminal-modified huAFD.v2.13 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFKNEFKSRATLTVDSTSTAYLELSSLRSEDVAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSVERK
10	SEQ ID NO: 620	C' terminal-modified huAFD.v2.14 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFKNEFKSRATLTVDSTSTAYLELSSLRSEDVAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSVERK
15	SEQ ID NO: 621	C' terminal-modified huAFD.v2.15 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPYSGETNFKNEFKSRATLTVDSTSTAYLELSSLRSEDVAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSVERK
20	SEQ ID NO: 622	C' terminal-modified AFD WT Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREKG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSVERKC
25	SEQ ID NO: 623	C' terminal-modified AFD.v1 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREKG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSVERKC
30	SEQ ID NO: 624	C' terminal-modified AFD.v2 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREKG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSVERKC
35	SEQ ID NO: 625	C' terminal-modified AFD.v3 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREKG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSVERKC
40	SEQ ID NO: 626	C' terminal-modified AFD.v4 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREKG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSVERKC
45	SEQ ID NO: 627	C' terminal-modified AFD.v5 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREKG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSVERKC
50	SEQ ID NO: 628	C' terminal-modified AFD.v6 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREKG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSVERKC

(continued)

5	SEQ ID NO: 629	C' terminal-modified AFD.v7 Heavy Chain	EVQLVQSGPELKKPGASVKVSCASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSVERKC
10	SEQ ID NO: 630	C' terminal-modified AFD.v8 Heavy Chain	EVQLVQSGPELKKPGASVKVSCASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSVERKC
15	SEQ ID NO: 631	C' terminal-modified AFD.v9 Heavy Chain	EVQLVQSGPELKKPGASVKVSCASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSVERKC
20	SEQ ID NO: 632	C' terminal-modified AFD.v10 Heavy Chain	EVQLVQSGPELKKPGASVKVSCASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSVERKC
25	SEQ ID NO: 633	C' terminal-modified AFD.v11 Heavy Chain	EVQLVQSGPELKKPGASVKVSCASGYTFTNYGMNWVRQAPGQGLEWMG WISTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSVERKC
30	SEQ ID NO: 634	C' terminal-modified AFD.v12 Heavy Chain	EVQLVQSGPELKKPGASVKVSCASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VDNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSVERKC
35	SEQ ID NO: 635	C' terminal-modified AFD.v13 Heavy Chain	EVQLVQSGPELKKPGASVKVSCASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VQNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSVERKC
40	SEQ ID NO: 636	C' terminal-modified AFD.v14 Heavy Chain	EVQLVQSGPELKKPGASVKVSCASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VSNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSVERKC
45	SEQ ID NO: 637	C' terminal-modified AFD.v15 Heavy Chain	EVQLVQSGPELKKPGASVKVSCASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VSNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSVERKC
50	SEQ ID NO: 638	C' terminal-modified huAFD.v2.0 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFKNEFKSRATLTVDSTSTAYLELSSLRSED TAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSVERKC

(continued)

5	SEQ ID NO: 639	C' terminal-modified huAFD.v2.1 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDSTSTAYLELSSLRSEDNAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSVERKC
10	SEQ ID NO: 640	C' terminal-modified huAFD.v2.3 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPYSGDTNFNEKFKSRATLTVDSTSTAYLELSSLRSEDNAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSVERKC
15	SEQ ID NO: 641	C' terminal-modified huAFD.v1 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTNGGTNFNEKFKSRATLTVDSTSTAYLELSSLRSEDNAVYYCAREGGF AYWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSVERKC
20	SEQ ID NO: 642	C' terminal-modified huAFD.v1.1 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTQGGTNFNEKFKSRATLTVDSTSTAYLELSSLRSEDNAVYYCAREGGF AYWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSVERKC
25	SEQ ID NO: 643	C' terminal-modified huAFD.v2.2 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGDTNFNEKFKSRATLTVDSTSTAYLELSSLRSEDNAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSVERKC
30	SEQ ID NO: 644	C' terminal-modified huAFD.v2.4 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGETNFNEKFKSRATLTVDSTSTAYLELSSLRSEDNAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSVERKC
35	SEQ ID NO: 645	C' terminal-modified huAFD.v2.5 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPYSGGTNFNEKFKSRATLTVDSTSTAYLELSSLRSEDNAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSVERKC
40	SEQ ID NO: 646	C' terminal-modified huAFD.v2.6 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDSTSTAYLELSSLRSEDNAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSVERKC
45	SEQ ID NO: 647	C' terminal-modified huAFD.v2.7 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDSTSTAYLELSSLRSEDNAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSVERKC
50	SEQ ID NO: 648	C' terminal-modified huAFD.v2.8 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDSTSTAYLELSSLRSEDNAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSVERKC

(continued)

5	SEQ ID NO: 649	C' terminal-modified huAFD.v2.9 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIG WINPTSGGTNFNEKFKSRATLTVDVTSTSTAYLELSSLRSED ~~T~~ AVYYCAREGG FAYWGQGT ~~L~~ LVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSVERKC
10	SEQ ID NO: 650	C' terminal-modified huAFD.v2.10 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDVTSTSTAYLELSSLRSED ~~T~~ AVYYCAREGGFA YWGQGT ~~L~~ LVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSVERKC
15	SEQ ID NO: 651	C' terminal-modified huAFD.v2.11 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDVTSTSTAYLELSSLRSED ~~T~~ AVYYCAREGGFA YWGQGT ~~L~~ LVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSVERKC
20	SEQ ID NO: 652	C' terminal-modified huAFD.v2.12 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPYSGGTNFNEKFKSRATLTVDVTSTSTAYLELSSLRSED ~~T~~ AVYYCAREGGFA YWGQGT ~~L~~ LVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSVERKC
25	SEQ ID NO: 653	C' terminal-modified huAFD.v2.13 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDVTSTSTAYLELSSLRSED ~~T~~ AVYYCAREGGFA YWGQGT ~~L~~ LVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSVERKC
30	SEQ ID NO: 654	C' terminal-modified huAFD.v2.14 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGETNFNEKFKSRATLTVDVTSTSTAYLELSSLRSED ~~T~~ AVYYCAREGGFA YWGQGT ~~L~~ LVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSVERKC
35	SEQ ID NO: 655	C' terminal-modified huAFD.v2.15 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPYSGETNFNEKFKSRATLTVDVTSTSTAYLELSSLRSED ~~T~~ AVYYCAREGGFA YWGQGT ~~L~~ LVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSVERKC
40	SEQ ID NO: 656	C' terminal-modified AFD WT Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGT ~~L~~ LVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSKYGPPC
45	SEQ ID NO: 657	C' terminal-modified AFD.v1 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGT ~~L~~ LVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSKYGPPC
50	SEQ ID NO: 658	C' terminal-modified AFD.v2 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGT ~~L~~ LVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSKYGPPC
55	SEQ ID NO: 658	C' terminal-modified AFD.v2 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGT ~~L~~ LVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSKYGPPC

(continued)

5	SEQ ID NO: 659	C' terminal- modified AFD.v3 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSKYGPCC
10	SEQ ID NO: 660	C' terminal- modified AFD.v4 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSKYGPCC
15	SEQ ID NO: 661	C' terminal- modified AFD.v5 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSKYGPCC
20	SEQ ID NO: 662	C' terminal- modified AFD.v6 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSKYGPCC
25	SEQ ID NO: 663	C' terminal- modified AFD.v7 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSKYGPCC
30	SEQ ID NO: 664	C' terminal- modified AFD.v8 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSKYGPCC
35	SEQ ID NO: 665	C' terminal- modified AFD.v9 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSKYGPCC
40	SEQ ID NO: 666	C' terminal- modified AFD.v10 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSKYGPCC
45	SEQ ID NO: 667	C' terminal- modified AFD.v11 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWRQAPGQGLEWMG WISTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSKYGPCC
50	SEQ ID NO: 668	C' terminal- modified AFD.v12 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VDNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSKYGPCC

(continued)

5	SEQ ID NO: 669	C' terminal-modified AFD.v13 Heavy Chain	EVQLVQSGPELKKPGASVKVSCASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEEDTAVYYCEREGLG VQNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSKYGPCC
10	SEQ ID NO: 670	C' terminal-modified AFD.v14 Heavy Chain	EVQLVQSGPELKKPGASVKVSCASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEEDTAVYYCEREGLG VSNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSKYGPCC
15	SEQ ID NO: 671	C' terminal-modified AFD.v15 Heavy Chain	EVQLVQSGPELKKPGASVKVSCASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEEDTAVYYCEREGLG VSNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSKYGPCC
20	SEQ ID NO: 672	C' terminal-modified huAFD.v2.0 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFKNEFKSRATLTVDTSSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSKYGPCC
25	SEQ ID NO: 673	C' terminal-modified huAFD.v2.1 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFKNEFKSRATLTVDTSSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSKYGPCC
30	SEQ ID NO: 674	C' terminal-modified huAFD.v2.3 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCASGYTFTSYMYWVRQAPGQGLEWIGE INPYSGDTNFKNEFKSRATLTVDTSSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSKYGPCC
35	SEQ ID NO: 675	C' terminal-modified huAFD.v1 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCASGYTFTSYMYWVRQAPGQGLEWIGE INPTNGGTNFKNEFKSRATLTVDTSSTAYLELSSLRSEDTAVYYCAREGGF AYWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSKYGPCC
40	SEQ ID NO: 676	C' terminal-modified huAFD.v1.1 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCASGYTFTSYMYWVRQAPGQGLEWIGE INPTQGGTNFKNEFKSRATLTVDTSSTAYLELSSLRSEDTAVYYCAREGGF AYWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSKYGPCC
45	SEQ ID NO: 677	C' terminal-modified huAFD.v2.2 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGDTNFKNEFKSRATLTVDTSSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSKYGPCC
50	SEQ ID NO: 678	C' terminal-modified huAFD.v2.4 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGDTNFKNEFKSRATLTVDTSSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSKYGPCC

(continued)

5	SEQ ID NO: 679	C' terminal-modified huAFD.v2.5 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPYSGGTNFKNEKFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSKYGPCC
10	SEQ ID NO: 680	C' terminal-modified huAFD.v2.6 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFKNEKFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSKYGPCC
15	SEQ ID NO: 681	C' terminal-modified huAFD.v2.7 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFKNEKFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSKYGPCC
20	SEQ ID NO: 682	C' terminal-modified huAFD.v2.8 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFKNEKFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSKYGPCC
25	SEQ ID NO: 683	C' terminal-modified huAFD.v2.9 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIG WINPTSGGTNFKNEKFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGG FAYWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSKYGPCC
30	SEQ ID NO: 684	C' terminal-modified huAFD.v2.10 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFKNEKFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSKYGPCC
35	SEQ ID NO: 685	C' terminal-modified huAFD.v2.11 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFKNEKFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSKYGPCC
40	SEQ ID NO: 686	C' terminal-modified huAFD.v2.12 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPYSGGTNFKNEKFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSKYGPCC
45	SEQ ID NO: 687	C' terminal-modified huAFD.v2.13 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFKNEKFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSKYGPCC
50	SEQ ID NO: 688	C' terminal-modified huAFD.v2.14 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFKNEKFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSKYGPCC

(continued)

5	SEQ ID NO: 689	C' terminal-modified huAFD.v2.15 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPYSGETNFNEKFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSKYGGP
10	SEQ ID NO: 690	C' terminal-modified AFD WT Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSKYGGP
15	SEQ ID NO: 691	C' terminal-modified AFD.v1 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSKYGGP
20	SEQ ID NO: 692	C' terminal-modified AFD.v2 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSKYGGP
25	SEQ ID NO: 693	C' terminal-modified AFD.v3 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSKYGGP
30	SEQ ID NO: 694	C' terminal-modified AFD.v4 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSKYGGP
35	SEQ ID NO: 695	C' terminal-modified AFD.v5 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSKYGGP
40	SEQ ID NO: 696	C' terminal-modified AFD.v6 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSKYGGP
45	SEQ ID NO: 697	C' terminal-modified AFD.v7 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSKYGGP
50	SEQ ID NO: 698	C' terminal-modified AFD.v8 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSKYGGP

(continued)

5	SEQ ID NO: 699	C' terminal-modified AFD.v9 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSSLKAEDTAVYYCEREGL VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSKYGP
10	SEQ ID NO: 700	C' terminal-modified AFD.v10 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSSLKAEDTAVYYCEREGL VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSKYGP
15	SEQ ID NO: 701	C' terminal-modified AFD.v11 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWRQAPGQGLEWMG WISTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSSLKAEDTAVYYCEREGL VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSKYGP
20	SEQ ID NO: 702	C' terminal-modified AFD.v12 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSSLKAEDTAVYYCEREGL VDNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSKYGP
25	SEQ ID NO: 703	C' terminal-modified AFD.v13 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSSLKAEDTAVYYCEREGL VQNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSKYGP
30	SEQ ID NO: 704	C' terminal-modified AFD.v14 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSSLKAEDTAVYYCEREGL VSNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSKYGP
35	SEQ ID NO: 705	C' terminal-modified AFD.v15 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSSLKAEDTAVYYCEREGL VSNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSKYGP
40	SEQ ID NO: 706	C' terminal-modified huAFD.v2.0 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFKNEFKSRATLTVDSTSTAYLELSSLRSED TAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSKYGP
45	SEQ ID NO: 707	C' terminal-modified huAFD.v2.1 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFKNEFKSRATLTVDSTSTAYLELSSLRSED TAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSKYGP
50	SEQ ID NO: 708	C' terminal-modified huAFD.v2.3 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPYSGDTNFKNEFKSRATLTVDSTSTAYLELSSLRSED TAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSKYGP

(continued)

5	SEQ ID NO: 709	C' terminal-modified huAFD.v1 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTNGGTNFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGF AYWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSKYGP
10	SEQ ID NO: 710	C' terminal-modified huAFD.v1.1 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTQGGTNFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGF AYWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSKYGP
15	SEQ ID NO: 711	C' terminal-modified huAFD.v2.2 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGDTNFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSKYGP
20	SEQ ID NO: 712	C' terminal-modified huAFD.v2.4 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGETNFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSKYGP
25	SEQ ID NO: 713	C' terminal-modified huAFD.v2.5 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPYSGGTNFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSKYGP
30	SEQ ID NO: 714	C' terminal-modified huAFD.v2.6 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSKYGP
35	SEQ ID NO: 715	C' terminal-modified huAFD.v2.7 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSKYGP
40	SEQ ID NO: 716	C' terminal-modified huAFD.v2.8 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSKYGP
45	SEQ ID NO: 717	C' terminal-modified huAFD.v2.9 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIG WINPTSGGTNFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGG FAYWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSKYGP
50	SEQ ID NO: 718	C' terminal-modified huAFD.v2.10 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSKYGP

(continued)

5	SEQ ID NO: 719	C' terminal-modified huAFD.v2.11 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFKNEKFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSKYGP
10	SEQ ID NO: 720	C' terminal-modified huAFD.v2.12 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPYSGGTNFKNEKFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSKYGP
15	SEQ ID NO: 721	C' terminal-modified huAFD.v2.13 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFKNEKFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSKYGP
20	SEQ ID NO: 722	C' terminal-modified huAFD.v2.14 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFKNEKFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSKYGP
25	SEQ ID NO: 723	C' terminal-modified huAFD.v2.15 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPYSGGTNFKNEKFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSKYGP
30	SEQ ID NO: 724	C' terminal-modified AFD WT Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREKG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSKYGP
35	SEQ ID NO: 725	C' terminal-modified AFD.v1 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREKG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSKYGP
40	SEQ ID NO: 726	C' terminal-modified AFD.v2 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREKG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSKYGP
45	SEQ ID NO: 727	C' terminal-modified AFD.v3 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREKG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSKYGP
50	SEQ ID NO: 728	C' terminal-modified AFD.v4 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREKG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSKYGP

(continued)

5	SEQ ID NO: 729	C' terminal-modified AFD.v5 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWRQAPGGGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSKYGP
10	SEQ ID NO: 730	C' terminal-modified AFD.v6 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWRQAPGGGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSKYGP
15	SEQ ID NO: 731	C' terminal-modified AFD.v7 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWRQAPGGGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSKYGP
20	SEQ ID NO: 732	C' terminal-modified AFD.v8 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWRQAPGGGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSKYGP
25	SEQ ID NO: 733	C' terminal-modified AFD.v9 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWRQAPGGGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSKYGP
30	SEQ ID NO: 734	C' terminal-modified AFD.v10 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWRQAPGGGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSKYGP
35	SEQ ID NO: 735	C' terminal-modified AFD.v11 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWRQAPGGGLEWMG WISTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSKYGP
40	SEQ ID NO: 736	C' terminal-modified AFD.v12 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWRQAPGGGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VDNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSKYGP
45	SEQ ID NO: 737	C' terminal-modified AFD.v13 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWRQAPGGGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VQNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSKYGP
50	SEQ ID NO: 738	C' terminal-modified AFD.v14 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWRQAPGGGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VSNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSKYGP

(continued)

5	SEQ ID NO: 739	C' terminal-modified AFD.v15 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VSNWQGGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSKYGP
10	SEQ ID NO: 740	C' terminal-modified huAFD.v2.0 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDTSSTAYLELSSLRSEDVAVYYCAREGGFA YWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSKYGP
15	SEQ ID NO: 741	C' terminal-modified huAFD.v2.1 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDTSSTAYLELSSLRSEDVAVYYCAREGGFA YWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSKYGP
20	SEQ ID NO: 742	C' terminal-modified huAFD.v2.3 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPYSGDTNFNEKFKSRATLTVDTSSTAYLELSSLRSEDVAVYYCAREGGFA YWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSKYGP
25	SEQ ID NO: 743	C' terminal-modified huAFD.v1 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTNGGTNFNEKFKSRATLTVDTSSTAYLELSSLRSEDVAVYYCAREGGF AYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSKYGP
30	SEQ ID NO: 744	C' terminal-modified huAFD.v1.1 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTQGGTNFNEKFKSRATLTVDTSSTAYLELSSLRSEDVAVYYCAREGGF AYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSKYGP
35	SEQ ID NO: 745	C' terminal-modified huAFD.v2.2 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGDTNFNEKFKSRATLTVDTSSTAYLELSSLRSEDVAVYYCAREGGFA YWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSKYGP
40	SEQ ID NO: 746	C' terminal-modified huAFD.v2.4 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGETNFNEKFKSRATLTVDTSSTAYLELSSLRSEDVAVYYCAREGGFA YWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSKYGP
45	SEQ ID NO: 747	C' terminal-modified huAFD.v2.5 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPYSGGTNFNEKFKSRATLTVDTSSTAYLELSSLRSEDVAVYYCAREGGFA YWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSKYGP
50	SEQ ID NO: 748	C' terminal-modified huAFD.v2.6 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDTSSTAYLELSSLRSEDVAVYYCAREGGFA YWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSKYGP

(continued)

5	SEQ ID NO: 749	C' terminal- modified huAFD.v2.7 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDLTSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSKYGP
10	SEQ ID NO: 750	C' terminal- modified huAFD.v2.8 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDLTSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSKYGP
15	SEQ ID NO: 751	C' terminal- modified huAFD.v2.9 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIG WINPTSGGTNFNEKFKSRATLTVDLTSTSTAYLELSSLRSEDTAVYYCAREGG FAYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSKYGP
20	SEQ ID NO: 752	C' terminal- modified huAFD.v2.10 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDLTSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSKYGP
25	SEQ ID NO: 753	C' terminal- modified huAFD.v2.11 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDLTSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSKYGP
30	SEQ ID NO: 754	C' terminal- modified huAFD.v2.12 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPYSGGTNFNEKFKSRATLTVDLTSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSKYGP
35	SEQ ID NO: 755	C' terminal- modified huAFD.v2.13 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDLTSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSKYGP
40	SEQ ID NO: 756	C' terminal- modified huAFD.v2.14 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDLTSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSKYGP
45	SEQ ID NO: 757	C' terminal- modified huAFD.v2.15 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPYSGETNFNEKFKSRATLTVDLTSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSKYGP
50	SEQ ID NO: 758	C' terminal- modified AFD WT Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCAREGG VNNWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSKYGP

(continued)

5	SEQ ID NO: 759	C' terminal- modified AFD.v1 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSKYG
10	SEQ ID NO: 760	C' terminal- modified AFD.v2 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSKYG
15	SEQ ID NO: 761	C' terminal- modified AFD.v3 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSKYG
20	SEQ ID NO: 762	C' terminal- modified AFD.v4 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSKYG
25	SEQ ID NO: 763	C' terminal- modified AFD.v5 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSKYG
30	SEQ ID NO: 764	C' terminal- modified AFD.v6 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSKYG
35	SEQ ID NO: 765	C' terminal- modified AFD.v7 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSKYG
40	SEQ ID NO: 766	C' terminal- modified AFD.v8 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSKYG
45	SEQ ID NO: 767	C' terminal- modified AFD.v9 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSKYG
50	SEQ ID NO: 768	C' terminal- modified AFD.v10 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSKYG

(continued)

5	SEQ ID NO: 769	C' terminal- modified AFD.v11 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WISTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGL VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSKYG
10	SEQ ID NO: 770	C' terminal- modified AFD.v12 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGL VDNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSKYG
15	SEQ ID NO: 771	C' terminal- modified AFD.v13 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGL VQNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSKYG
20	SEQ ID NO: 772	C' terminal- modified AFD.v14 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGL VSNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSKYG
25	SEQ ID NO: 773	C' terminal- modified AFD.v15 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGL VSNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSKYG
30	SEQ ID NO: 774	C' terminal- modified huAFD.v2.0 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFKNEFKSRATLTVDSTSTAYLELSSLRSED TAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSKYG
35	SEQ ID NO: 775	C' terminal- modified huAFD.v2.1 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFKNEFKSRATLTVDSTSTAYLELSSLRSED TAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSKYG
40	SEQ ID NO: 776	C' terminal- modified huAFD.v2.3 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPYS GDTNFKNEFKSRATLTVDSTSTAYLELSSLRSED TAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSKYG
45	SEQ ID NO: 777	C' terminal- modified huAFD.v1 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTNGGTNFKNEFKSRATLTVDSTSTAYLELSSLRSED TAVYYCAREGGF AYWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSKYG
50	SEQ ID NO: 778	C' terminal- modified huAFD.v1.1 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTQGGTNFKNEFKSRATLTVDSTSTAYLELSSLRSED TAVYYCAREGGF AYWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSKYG

(continued)

5	SEQ ID NO: 779	C' terminal- modified huAFD.v2.2 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGDTNFNEKFKSRATLTVDLTSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSKYG
10	SEQ ID NO: 780	C' terminal- modified huAFD.v2.4 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGETNFNEKFKSRATLTVDLTSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSKYG
15	SEQ ID NO: 781	C' terminal- modified huAFD.v2.5 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPYSGGTNFNEKFKSRATLTVDLTSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSKYG
20	SEQ ID NO: 782	C' terminal- modified huAFD.v2.6 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDLTSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSKYG
25	SEQ ID NO: 783	C' terminal- modified huAFD.v2.7 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDLTSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSKYG
30	SEQ ID NO: 784	C' terminal- modified huAFD.v2.8 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDLTSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSKYG
35	SEQ ID NO: 785	C' terminal- modified huAFD.v2.9 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIG WINPTSGGTNFNEKFKSRATLTVDLTSTSTAYLELSSLRSEDTAVYYCAREGG FAYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSKYG
40	SEQ ID NO: 786	C' terminal- modified huAFD.v2.10 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDLTSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSKYG
45	SEQ ID NO: 787	C' terminal- modified huAFD.v2.11 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDLTSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSKYG
50	SEQ ID NO: 788	C' terminal- modified huAFD.v2.12 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPYSGGTNFNEKFKSRATLTVDLTSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSKYG

(continued)

5	SEQ ID NO: 789	C' terminal-modified huAFD.v2.13 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSKY
10	SEQ ID NO: 790	C' terminal-modified huAFD.v2.14 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSKY
15	SEQ ID NO: 791	C' terminal-modified huAFD.v2.15 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSKY
20	SEQ ID NO: 792	C' terminal-modified AFD WT Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCERE GGVNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSKY
25	SEQ ID NO: 793	C' terminal-modified AFD.v1 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCERE GGVNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSKY
30	SEQ ID NO: 794	C' terminal-modified AFD.v2 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCERE GGVNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSKY
35	SEQ ID NO: 795	C' terminal-modified AFD.v3 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCERE GGVNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSKY
40	SEQ ID NO: 796	C' terminal-modified AFD.v4 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCERE GGVNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSKY
45	SEQ ID NO: 797	C' terminal-modified AFD.v5 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCERE GGVNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSKY
50	SEQ ID NO: 798	C' terminal-modified AFD.v6 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCERE GGVNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSKY

(continued)

5	SEQ ID NO: 799	C' terminal-modified AFD.v7 Heavy Chain	EVQLVQSGPELKKPGASVKV SCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGT LTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSKY
10	SEQ ID NO: 800	C' terminal-modified AFD.v8 Heavy Chain	EVQLVQSGPELKKPGASVKV SCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGT LTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSKY
15	SEQ ID NO: 801	C' terminal-modified AFD.v9 Heavy Chain	EVQLVQSGPELKKPGASVKV SCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGT LTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSKY
20	SEQ ID NO: 802	C' terminal-modified AFD.v10 Heavy Chain	EVQLVQSGPELKKPGASVKV SCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGT LTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSKY
25	SEQ ID NO: 803	C' terminal-modified AFD.v11 Heavy Chain	EVQLVQSGPELKKPGASVKV SCKASGYTFTNYGMNWVRQAPGQGLEWMG WISTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGT LTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSKY
30	SEQ ID NO: 804	C' terminal-modified AFD.v12 Heavy Chain	EVQLVQSGPELKKPGASVKV SCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VDNWGQGT LTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSKY
35	SEQ ID NO: 805	C' terminal-modified AFD.v13 Heavy Chain	EVQLVQSGPELKKPGASVKV SCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VQNWGQGT LTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSKY
40	SEQ ID NO: 806	C' terminal-modified AFD.v14 Heavy Chain	EVQLVQSGPELKKPGASVKV SCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VSNWGQGT LTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSKY
45	SEQ ID NO: 807	C' terminal-modified AFD.v15 Heavy Chain	EVQLVQSGPELKKPGASVKV SCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VSNWGQGT LTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSKY
50	SEQ ID NO: 808	C' terminal-modified huAFD.v2.0 Heavy Chain	EVQLVQSGAEVKKPGASVKV SCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDSTSTAYLELSSLRSED TAVYYCAREGGFA YWGQGT LTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSKY

(continued)

5	SEQ ID NO: 809	C' terminal- modified huAFD.v2.1 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDLTSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSKY
10	SEQ ID NO: 810	C' terminal- modified huAFD.v2.3 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPYSGDTNFNEKFKSRATLTVDLTSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSKY
15	SEQ ID NO: 811	C' terminal- modified huAFD.v1 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTNGGTNFNEKFKSRATLTVDLTSTSTAYLELSSLRSEDTAVYYCAREGGF AYWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSKY
20	SEQ ID NO: 812	C' terminal- modified huAFD.v1.1 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTQGGTNFNEKFKSRATLTVDLTSTSTAYLELSSLRSEDTAVYYCAREGGF AYWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSKY
25	SEQ ID NO: 813	C' terminal- modified huAFD.v2.2 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGDTNFNEKFKSRATLTVDLTSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSKY
30	SEQ ID NO: 814	C' terminal- modified huAFD.v2.4 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGETNFNEKFKSRATLTVDLTSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSKY
35	SEQ ID NO: 815	C' terminal- modified huAFD.v2.5 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPYSGGTNFNEKFKSRATLTVDLTSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSKY
40	SEQ ID NO: 816	C' terminal- modified huAFD.v2.6 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDLTSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSKY
45	SEQ ID NO: 817	C' terminal- modified huAFD.v2.7 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDLTSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSKY
50	SEQ ID NO: 818	C' terminal- modified huAFD.v2.8 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDLTSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSKY

(continued)

5	SEQ ID NO: 819	C' terminal-modified huAFD.v2.9 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIG WINPTSGGTNFNEKFKSRATLTVDVTSTSTAYLELSSLRSEDVAVYYCAREGG FAYWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSKY
10	SEQ ID NO: 820	C' terminal-modified huAFD.v2.10 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDVTSTSTAYLELSSLRSEDVAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSKY
15	SEQ ID NO: 821	C' terminal-modified huAFD.v2.11 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDVTSTSTAYLELSSLRSEDVAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSKY
20	SEQ ID NO: 822	C' terminal-modified huAFD.v2.12 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPYSGGTNFNEKFKSRATLTVDVTSTSTAYLELSSLRSEDVAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSKY
25	SEQ ID NO: 823	C' terminal-modified huAFD.v2.13 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDVTSTSTAYLELSSLRSEDVAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSKY
30	SEQ ID NO: 824	C' terminal-modified huAFD.v2.14 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFNEKFKSRATLTVDVTSTSTAYLELSSLRSEDVAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSKY
35	SEQ ID NO: 825	C' terminal-modified huAFD.v2.15 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPYSGGTNFNEKFKSRATLTVDVTSTSTAYLELSSLRSEDVAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSKY
40	SEQ ID NO: 826	C' terminal-modified AFD WT Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREKG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSK
45	SEQ ID NO: 827	C' terminal-modified AFD.v1 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREKG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSK
50	SEQ ID NO: 828	C' terminal-modified AFD.v2 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREKG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSK
55	SEQ ID NO: 828	C' terminal-modified AFD.v2 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREKG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSK

(continued)

5	SEQ ID NO: 829	C' terminal- modified AFD.v3 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSK
10	SEQ ID NO: 830	C' terminal- modified AFD.v4 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSK
15	SEQ ID NO: 831	C' terminal- modified AFD.v5 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSK
20	SEQ ID NO: 832	C' terminal- modified AFD.v6 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSK
25	SEQ ID NO: 833	C' terminal- modified AFD.v7 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSK
30	SEQ ID NO: 834	C' terminal- modified AFD.v8 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSK
35	SEQ ID NO: 835	C' terminal- modified AFD.v9 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSK
40	SEQ ID NO: 836	C' terminal- modified AFD.v10 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSK
45	SEQ ID NO: 837	C' terminal- modified AFD.v11 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWRQAPGQGLEWMG WISTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSK
50	SEQ ID NO: 838	C' terminal- modified AFD.v12 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VDNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSK

(continued)

5	SEQ ID NO: 839	C' terminal-modified AFD.v13 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEEDTAVYYCEREGLG VQNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSK
10	SEQ ID NO: 840	C' terminal-modified AFD.v14 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEEDTAVYYCEREGLG VSNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSK
15	SEQ ID NO: 841	C' terminal-modified AFD.v15 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEEDTAVYYCEREGLG VSNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSK
20	SEQ ID NO: 842	C' terminal-modified huAFD.v2.0 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFKNEFKSRATLTVDTSSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSK
25	SEQ ID NO: 843	C' terminal-modified huAFD.v2.1 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFKNEFKSRATLTVDTSSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSK
30	SEQ ID NO: 844	C' terminal-modified huAFD.v2.3 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPYSGDTNFKNEFKSRATLTVDTSSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSK
35	SEQ ID NO: 845	C' terminal-modified huAFD.v1 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTNGGTNFKNEFKSRATLTVDTSSTAYLELSSLRSEDTAVYYCAREGGF AYWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSK
40	SEQ ID NO: 846	C' terminal-modified huAFD.v1.1 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTQGGTNFKNEFKSRATLTVDTSSTAYLELSSLRSEDTAVYYCAREGGF AYWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSK
45	SEQ ID NO: 847	C' terminal-modified huAFD.v2.2 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGDTNFKNEFKSRATLTVDTSSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSK
50	SEQ ID NO: 848	C' terminal-modified huAFD.v2.4 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGDTNFKNEFKSRATLTVDTSSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSK

(continued)

5	SEQ ID NO: 849	C' terminal- modified huAFD.v2.5 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPYSGGTNFKNEKFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSK
10	SEQ ID NO: 850	C' terminal- modified huAFD.v2.6 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFKNEKFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSK
15	SEQ ID NO: 851	C' terminal- modified huAFD.v2.7 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFKNEKFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSK
20	SEQ ID NO: 852	C' terminal- modified huAFD.v2.8 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFKNEKFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSK
25	SEQ ID NO: 853	C' terminal- modified huAFD.v2.9 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIG WINPTSGGTNFKNEKFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGG FAYWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSK
30	SEQ ID NO: 854	C' terminal- modified huAFD.v2.10 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFKNEKFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSK
35	SEQ ID NO: 855	C' terminal- modified huAFD.v2.11 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFKNEKFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSK
40	SEQ ID NO: 856	C' terminal- modified huAFD.v2.12 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPYSGGTNFKNEKFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSK
45	SEQ ID NO: 857	C' terminal- modified huAFD.v2.13 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFKNEKFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSK
50	SEQ ID NO: 858	C' terminal- modified huAFD.v2.14 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFKNEKFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSK

(continued)

5	SEQ ID NO: 859	C' terminal-modified huAFD.v2.15 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPYSGETNFNEKFKSRATLTVDSTSTAYLELSSLRSEDTAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSK
10	SEQ ID NO: 882	C' terminal-modified AFD WT Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSKCDKTHX (X is any amino acid except T)
15	SEQ ID NO: 883	C' terminal-modified AFD.v1 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSKCDKTHX (X is any amino acid except T)
20	SEQ ID NO: 884	C' terminal-modified AFD.v2 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSKCDKTHX (X is any amino acid except T)
25	SEQ ID NO: 885	C' terminal-modified AFD.v3 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSKCDKTHX (X is any amino acid except T)
30	SEQ ID NO: 886	C' terminal-modified AFD.v4 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSKCDKTHX (X is any amino acid except T)
35	SEQ ID NO: 887	C' terminal-modified AFD.v5 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSKCDKTHX (X is any amino acid except T)
40	SEQ ID NO: 888	C' terminal-modified AFD.v6 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSKCDKTHX (X is any amino acid except T)
45	SEQ ID NO: 889	C' terminal-modified AFD.v7 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSKCDKTHX (X is any amino acid except T)

55

(continued)

5	SEQ ID NO: 890	C' terminal- modified AFD.v8 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGLG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHX (X is any amino acid except T)
10	SEQ ID NO: 891	C' terminal- modified AFD.v9 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGLG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHX (X is any amino acid except T)
15	SEQ ID NO: 892	C' terminal- modified AFD.v10 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGLG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHX (X is any amino acid except T)
20	SEQ ID NO: 893	C' terminal- modified AFD.v11 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWRQAPGQGLEWMG WISTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGLG VNNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHX (X is any amino acid except T)
25	SEQ ID NO: 894	C' terminal- modified AFD.v12 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGLG VDNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHX (X is any amino acid except T)
30	SEQ ID NO: 895	C' terminal- modified AFD.v13 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGLG VQNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHX (X is any amino acid except T)
35	SEQ ID NO: 896	C' terminal- modified AFD.v14 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGLG VSNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHX (X is any amino acid except T)
40	SEQ ID NO: 897	C' terminal- modified AFD.v15 Heavy Chain	EVQLVQSGPELKKPGASVKVSCKASGYTFTNYGMNWRQAPGQGLEWMG WINTYTGETTYAEDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCEREGLG VSNWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHX (X is any amino acid except T)
45	SEQ ID NO: 898	C' terminal- modified huAFD.v2.0 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFKNEFKSRATLTVDTSSTAYLELSSLRSED TAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHX (X is any amino acid except T)

(continued)

5	SEQ ID NO: 899	C' terminal-modified huAFD.v2.1 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFKNEKFKSRATLTVDSTSTAYLELSSLRSEDVAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHX (X is any amino acid except T)
10	SEQ ID NO: 900	C' terminal-modified huAFD.v2.3 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPYSGDTNFKNEKFKSRATLTVDSTSTAYLELSSLRSEDVAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHX (X is any amino acid except T)
15	SEQ ID NO: 901	C' terminal-modified huAFD.v1 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTNGGTNFKNEKFKSRATLTVDSTSTAYLELSSLRSEDVAVYYCAREGGF AYWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSCDKTHX (X is any amino acid except T)
20	SEQ ID NO: 902	C' terminal-modified huAFD.v1.1 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTQGGTNFKNEKFKSRATLTVDSTSTAYLELSSLRSEDVAVYYCAREGGF AYWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSCDKTHX (X is any amino acid except T)
25	SEQ ID NO: 903	C' terminal-modified huAFD.v2.2 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGDTNFKNEKFKSRATLTVDSTSTAYLELSSLRSEDVAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHX (X is any amino acid except T)
30	SEQ ID NO: 904	C' terminal-modified huAFD.v2.4 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGETNFKNEKFKSRATLTVDSTSTAYLELSSLRSEDVAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHX (X is any amino acid except T)
35	SEQ ID NO: 905	C' terminal-modified huAFD.v2.5 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPYSGGTNFKNEKFKSRATLTVDSTSTAYLELSSLRSEDVAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHX (X is any amino acid except T)
40	SEQ ID NO: 906	C' terminal-modified huAFD.v2.6 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFKNEKFKSRATLTVDSTSTAYLELSSLRSEDVAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHX (X is any amino acid except T)
45	SEQ ID NO: 907	C' terminal-modified huAFD.v2.7 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIGE INPTSGGTNFKNEKFKSRATLTVDSTSTAYLELSSLRSEDVAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHX (X is any amino acid except T)

55

(continued)

5	SEQ ID NO: 908	C' terminal-modified huAFD.v2.8 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIG INPTSGGTNFNEKFKSRATLTVDLTSTSTAYLELSSLRSEDVAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHX (X is any amino acid except T)
10	SEQ ID NO: 909	C' terminal-modified huAFD.v2.9 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIG WINPTSGGTNFNEKFKSRATLTVDLTSTSTAYLELSSLRSEDVAVYYCAREGG FAYWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHX (X is any amino acid except T)
15	SEQ ID NO: 910	C' terminal-modified huAFD.v2.10 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIG INPTSGGTNFNEKFKSRATLTVDLTSTSTAYLELSSLRSEDVAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHX (X is any amino acid except T)
20	SEQ ID NO: 911	C' terminal-modified huAFD.v2.11 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIG INPTSGGTNFNEKFKSRATLTVDLTSTSTAYLELSSLRSEDVAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHX (X is any amino acid except T)
25	SEQ ID NO: 912	C' terminal-modified huAFD.v2.12 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIG INPYSGGTNFNEKFKSRATLTVDLTSTSTAYLELSSLRSEDVAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHX (X is any amino acid except T)
30	SEQ ID NO: 913	C' terminal-modified huAFD.v2.13 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIG INPTSGGTNFNEKFKSRATLTVDLTSTSTAYLELSSLRSEDVAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHX (X is any amino acid except T)
35	SEQ ID NO: 914	C' terminal-modified huAFD.v2.14 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIG INPTSGETNFNEKFKSRATLTVDLTSTSTAYLELSSLRSEDVAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHX (X is any amino acid except T)
40	SEQ ID NO: 915	C' terminal-modified huAFD.v2.15 Heavy Chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMYWVRQAPGQGLEWIG INPYSGETNFNEKFKSRATLTVDLTSTSTAYLELSSLRSEDVAVYYCAREGGFA YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHX (X is any amino acid except T)

[0433] In some embodiments, the anti-Factor D antibody is a Fab fragment, a Fab' fragment or a F(ab')₂ fragment comprising a light chain constant region having the amino acid sequence of SEQ ID NO: 860. In some embodiments, the anti-Factor D antibody is a Fab fragment, a Fab' fragment or a F(ab')₂ fragment comprising a light chain constant region having at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 860. See Table 9.

[0434] In some embodiments, the anti-Factor D antibody is a Fab fragment comprising a heavy chain constant region having the amino acid sequence of SEQ ID NO: 861, SEQ ID NO: 862, SEQ ID NO: 869, SEQ ID NO: 870, SEQ ID NO: 871, SEQ ID NO: 872, SEQ ID NO: 873, SEQ ID NO: 874, SEQ ID NO: 877, SEQ ID NO: 878, SEQ ID NO: 879, SEQ ID NO: 880, SEQ ID NO: 881, or SEQ ID NO: 916. In some embodiments, the anti-Factor D antibody is a Fab fragment, a Fab' fragment or a F(ab')₂ fragment comprising a heavy chain constant region having the amino acid sequence of

SEQ ID NO: 864, SEQ ID NO: 865, SEQ ID NO: 866, SEQ ID NO: 867, or SEQ ID NO: 868. In some embodiments, the anti-Factor D antibody is a Fab-C fragment comprising a heavy chain constant region having the amino acid sequence of SEQ ID NO: 863, SEQ ID NO: 875, or SEQ ID NO: 876. In some embodiments, the anti-Factor D antibody is a Fab fragment comprising a heavy chain constant region having at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 861, SEQ ID NO: 862, SEQ ID NO: 869, SEQ ID NO: 870, SEQ ID NO: 871, SEQ ID NO: 872, SEQ ID NO: 873, SEQ ID NO: 874, SEQ ID NO: 877, SEQ ID NO: 878, SEQ ID NO: 879, SEQ ID NO: 880, SEQ ID NO: 881, or SEQ ID NO: 916. In some embodiments, the anti-Factor D antibody is a Fab fragment, a Fab' fragment or a F(ab')₂ fragment comprising a heavy chain constant region having at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 864, SEQ ID NO: 865, SEQ ID NO: 866, SEQ ID NO: 867, or SEQ ID NO: 868. In some embodiments, the anti-Factor D antibody is a Fab-C fragment comprising a heavy chain constant region having at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 863, SEQ ID NO: 875, or SEQ ID NO: 876. See Table 9.

Table 9. Amino acid sequences of anti-Factor D antibody light chain constant regions and heavy chain constant regions

SEQ ID NO: 860	RTVAAPSVEFPPSDEQLKSGTASVVCLLNNFYBREAKVQWKVDNALQSGNSQESVTEQDKDSTYSLS STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
SEQ ID NO: 861	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVT VPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHT
SEQ ID NO: 862	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVT VPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHL
SEQ ID NO: 863	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVT VPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHIC
SEQ ID NO: 864	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVT VPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHICPPC
SEQ ID NO: 865	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVT VPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHICPPS
SEQ ID NO: 866	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVT VPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHISPPC
SEQ ID NO: 867	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVT VPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHIAPPC
SEQ ID NO: 868	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVT VPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHISGGC
SEQ ID NO: 869	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVT VPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCYGPCC
SEQ ID NO: 870	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVT VPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH
SEQ ID NO: 871	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVT VPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT

(continued)

SEQ ID NO: 872	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVT VPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDK
SEQ ID NO: 873	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVT VPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCD
SEQ ID NO: 874	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVT VPSSN FGTQTYTCNVDHKPSNTKVDKTVVERK
SEQ ID NO: 875	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVT VPSSN FGTQTYTCNVDHKPSNTKVDKTVVERKC
SEQ ID NO: 876	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVT VPSSSLGTKTYYTCNVVDHKPSNTKVDKRVESKYGPPC
SEQ ID NO: 877	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVT VPSSSLGTKTYYTCNVVDHKPSNTKVDKRVESKYGPP
SEQ ID NO: 878	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVT VPSSSLGTKTYYTCNVVDHKPSNTKVDKRVESKYG
SEQ ID NO: 879	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVT VPSSSLGTKTYYTCNVVDHKPSNTKVDKRVESKYG
SEQ ID NO: 880	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVT VPSSSLGTKTYYTCNVVDHKPSNTKVDKRVESKY
SEQ ID NO: 881	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVT VPSSSLGTKTYYTCNVVDHKPSNTKVDKRVESK
SEQ ID NO: 916	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVT VPSSS LGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHX (X is any amino acid except T)

[0435] In specific embodiments, the Factor D inhibitor is a small molecule inhibitor. In specific embodiments, the Factor D inhibitor is a nucleotide (e.g., a DNA, an RNA, an shRNA, an miRNA, an siRNA, an antisense DNA). In specific embodiments, the Factor D inhibitor is a peptide, a protein, a peptide mimetic, an aptamer, or any other molecule that binds to Factor D.

[0436] In the methods of determining the potency of a Factor D inhibitor described above, the anti-Factor Ba, anti-Factor Bb, and/or anti-Factor C3b may be replaced by a peptide, a non-antibody protein, a peptide mimetic, an aptamer, a nucleotide (e.g., DNA, RNA, shRNA, miRNA, siRNA, antisense DNA), or any other molecule that binds to Factor Ba, Factor Bb, or anti-Factor C3b, respectively. Alternatively, the Factor Ba, Factor Bb, and/or Factor C3b may be directed attached to the donor or acceptor (as the case may be) by direct chemical labeling.

[0437] In specific embodiments of the methods of determining the potency of a Factor D inhibitor described herein, the Factor D is a recombinantly expressed Factor D. In specific embodiments of the methods of determining the potency of a Factor D inhibitor described herein, the Factor D is endogenously expressed Factor D purified from a sample derived from a subject.

[0438] In specific embodiments of the methods of determining the potency of a Factor D inhibitor described herein, the Factor B is a recombinantly expressed Factor B. In specific embodiments of the methods of determining the potency of a Factor D inhibitor described herein, the Factor B is endogenously expressed Factor B purified from a sample derived from a subject.

[0439] The term "sample" referred to in the methods described herein, can be, but is not limited to, a blood sample or a serum sample.

[0440] The subject referred to in the methods described herein, can be, but is not limited to, a human or non-human vertebrate such as a wild, domestic or farm animal. In certain embodiments, the subject is a mammal, e.g., a human, a cow, a dog, a cat, a goat, a horse, a sheep, a pig, a rat, or a mouse. In a preferred embodiment, the subject is a human.

5.5. Methods of Screening for Factor D Inhibitors

[0441] In another aspect, provided herein are methods of screening for a Factor D inhibitor from a plurality of Factor D inhibitor candidates, comprising performing a proximity-based measurement assay, wherein the proximity-based measurement assay measures the cleavage of Factor B. The proximity-based measurement assay can utilize any proximity-based technology known in the art for measuring the binding of a protein pair, as described in Section 5.1. The methods described in this section are useful, for example, in high-throughput screening for new Factor D inhibitors.

[0442] In various embodiments, the methods of screening for a Factor D inhibitor comprise: (a) mixing a Factor D inhibitor candidate with Factor D, Factor B and Factor C3b in a test reaction mix; (b) incubating the test reaction mix; (c) adding to the test reaction mix an anti-Factor Ba antibody labeled with a first moiety and an anti-Factor Bb antibody labeled with a second moiety after the step of (b), wherein one of the moieties is a donor, and the other is an acceptor, and wherein a proximity signal generated by the acceptor and/or the donor indicates that Factor Ba and Factor Bb are in proximity; and (d) measuring the value of the proximity signal from the test reaction mix; wherein the degree of Factor D activity inhibition by a Factor D candidate is positively correlated with the value of the proximity signal. In certain embodiments, the steps of (a)-(d) are carried out for each Factor D inhibitor candidate from the plurality.

[0443] In certain aspects of such various embodiments, the methods of screening for a Factor D inhibitor further comprise: (e) mixing a control reaction mix; (f) incubating the control reaction mix; (g) adding to the control reaction mix the anti-Factor Ba antibody labeled with the first moiety and the anti-Factor Bb antibody labeled with the second moiety after the step of (f); and (h) measuring the value of the proximity signal from the control test reaction mix; wherein a greater value of the proximity signal from the test reaction mix relative to the control reaction mix (e.g., about 10%, 15%, 20%, 25%, 30%, 40%, 50%, 60%, 70%, 80%, 90% greater or more, or about 1-fold, 1.5-fold, 2-fold, 3-fold, 4-fold, 5-fold, 6-fold, 7-fold, 8-fold, 9-fold, 10-fold, 15-fold, 20-fold, 30-fold, 40-fold, 50-fold greater or more) indicates a greater inhibition of Factor D activity by the Factor D inhibitor candidate in the test reaction mix relative to the control reaction mix.

[0444] When the proximity signal generated by the donor and/or the acceptor is based on energy transfer between the donor and the acceptor upon light activation, in various embodiments, the methods of screening for a Factor D inhibitor comprise: (A) mixing a Factor D inhibitor candidate with Factor D, Factor B and Factor C3b in a test reaction mix; (B) incubating the test reaction mix; (C) adding to the test reaction mix an anti-Factor Ba antibody labeled with a first moiety and an anti-Factor Bb antibody labeled with a second moiety after the step of (B), wherein one of the moieties is a donor, and the other is an acceptor; (D) providing a light source to excite the donor in the test reaction mix; and (E) measuring the donor fluorescence emission intensity from the test reaction mix, and/or the acceptor fluorescence emission intensity from the test reaction mix; wherein the degree of Factor D activity inhibition by a Factor D candidate is negatively correlated with the donor fluorescence emission intensity from the test reaction mix, and/or is positively correlated with the acceptor fluorescence emission intensity from the test reaction mix. In specific embodiments, the step of (B) is conducted for about 15 min, 30 min, 45 min, 60 min, 75 min, or 90 min. In some embodiments, the step of (B) is conducted for about 45 min. In certain embodiments, the step of (E) is performed after a period of time of the step

of (D) that results in a decrease in interfering short-lived background signals. In specific embodiments, the methods of screening for a Factor D inhibitor further comprise: (F) mixing a control reaction mix; (G) incubating the control reaction mix; (H) adding to the control reaction mix the anti-Factor Ba antibody labeled with the first moiety and the anti-Factor Bb antibody labeled with the second moiety after the step of (G); (I) providing the same light source to excite the donor in the control reaction mix; and (J) measuring the donor fluorescence emission intensity from the control reaction mix, and/or the acceptor fluorescence emission intensity from the control reaction mix; wherein a lower donor fluorescence emission intensity from the test reaction mix relative to the control reaction mix, and/or a higher acceptor fluorescence emission intensity from the test reaction mix relative to the control reaction mix, indicates a greater inhibition of Factor D activity by the Factor D inhibitor candidate in the test reaction mix relative to the control reaction mix. In specific embodiments, the steps of (B) and (G) are conducted for about 15 min, 30 min, 45 min, 60 min, 75 min, or 90 min. In some embodiments, the steps of (B) and (G) are conducted for about 45 min. In certain embodiments, the step of (E) is performed after a period of time of the step of (D) that results in a decrease in interfering short-lived background signals, and the step of (J) is performed after the same period of time of the step of (J). In certain embodiments, the steps of (A)-(E) are carried out for each Factor D inhibitor candidate from the plurality.

[0445] In certain embodiments, the anti-Factor Ba antibody and the anti-Factor Bb antibody used in the methods of screening for a Factor D inhibitor quench the activity of Factor D. In such embodiments, the need to add another quencher specifically is obviated. In certain embodiments, the methods of screening for a Factor D inhibitor further comprise a step of quenching the activity of Factor D in the sample by providing an excessive amount of a quencher to the sample before the step of (c). When a control sample is used, in certain embodiments, the methods of screening for a Factor D inhibitor further comprise a step of quenching the activity of Factor D in the sample by providing an excessive amount of a quencher to the sample before the step of (c), and a step of quenching the activity of Factor D in the control sample by providing an excessive amount of the quencher to the control sample before the step of (g). In specific embodiments, the quencher is a Factor D inhibitor (for example, an anti-Factor D antibody or an excess amount of EDTA).

[0446] In certain embodiments, the anti-Factor Ba antibody is biotinylated, and the first moiety comprises streptavidin, avidin, or neutravidin. In some embodiments, the anti-Factor Ba antibody is biotinylated, and the first moiety comprises streptavidin. In certain embodiments, the anti-Factor Bb antibody is biotinylated, and the second moiety comprises streptavidin, avidin, or neutravidin. In some embodiments, the anti-Factor Bb antibody is biotinylated, and the second moiety comprises streptavidin.

[0447] In other various embodiments, the methods of screening for a Factor D inhibitor comprise: (a) mixing a Factor D inhibitor candidate with Factor D, Factor B and Factor C3b in a test reaction mix; (b) incubating the test reaction mix; (c) adding to the test reaction mix an anti-Factor C3b antibody labeled with a first moiety and an anti-Factor Ba antibody labeled with a second moiety after the step of (b), wherein one of the moieties is a donor, and the other is an acceptor, and wherein a proximity signal generated by the acceptor and/or the donor indicates that Factor C3b and Factor Ba are in proximity; and (d) measuring the value of the proximity signal from the test reaction mix; wherein the degree of Factor D activity inhibition by a Factor D candidate is positively correlated with the value of the proximity signal. In certain embodiments, the steps of (a)-(d) are carried out for each Factor D inhibitor candidate from the plurality.

[0448] In certain aspects of such other various embodiments, the methods of screening for a Factor D inhibitor further comprise: (e) mixing a control reaction mix; (f) incubating the control reaction mix; (g) adding to the control reaction mix the anti-Factor C3b antibody labeled with the first moiety and the anti-Factor Ba antibody labeled with the second moiety after the step of (f); and (h) measuring the value of the proximity signal from the control test reaction mix; wherein a greater value of the proximity signal from the test reaction mix relative to the control reaction mix (e.g., about 10%, 15%, 20%, 25%, 30%, 40%, 50%, 60%, 70%, 80%, 90% greater or more, or about 1-fold, 1.5-fold, 2-fold, 3-fold, 4-fold, 5-fold, 6-fold, 7-fold, 8-fold, 9-fold, 10-fold, 15-fold, 20-fold, 30-fold, 40-fold, 50-fold greater or more) indicates a greater inhibition of Factor D activity by the Factor D inhibitor candidate in the test reaction mix relative to the control reaction mix.

[0449] When the proximity signal generated by the donor and/or the acceptor is based on energy transfer between the donor and the acceptor upon light activation, in various embodiments, the methods of screening for a Factor D inhibitor comprise: (A) mixing a Factor D inhibitor candidate with Factor D, Factor B and Factor C3b in a test reaction mix; (B) incubating the test reaction mix; (C) adding to the test reaction mix an anti-Factor C3b antibody labeled with a first moiety and an anti-Factor Ba antibody labeled with a second moiety after the step of (B), wherein one of the moieties is a donor, and the other is an acceptor; (D) providing a light source to excite the donor in the test reaction mix; and (E) measuring the donor fluorescence emission intensity from the test reaction mix, and/or the acceptor fluorescence emission intensity from the test reaction mix; wherein the degree of Factor D activity inhibition by a Factor D candidate is negatively correlated with the donor fluorescence emission intensity from the test reaction mix, and/or is positively correlated with the acceptor fluorescence emission intensity from the test reaction mix. In specific embodiments, the step of (B) is conducted for about 15 min, 30 min, 45 min, 60 min, 75 min, or 90 min. In some embodiments, the step of (B) is conducted for about 45 min. In certain embodiments, the step of (E) is performed after a period of time of the step of (D) that results in a decrease in interfering short-lived background signals. In specific embodiments, the methods of screening for a Factor D inhibitor further comprise: (F) mixing a control reaction mix; (G) incubating the control reaction

mix; (H) adding to the control reaction mix the anti-Factor C3b antibody labeled with the first moiety and the anti-Factor Ba antibody labeled with the second moiety after the step of (G); (I) providing said light source to excite the donor in the control reaction mix; and (J) measuring the donor fluorescence emission intensity from the control reaction mix, and/or the acceptor fluorescence emission intensity from the control reaction mix; wherein a lower donor fluorescence emission intensity from the test reaction mix relative to the control reaction mix, and/or a higher acceptor fluorescence emission intensity from the test reaction mix relative to the control reaction mix, indicates a greater inhibition of Factor D activity by the Factor D inhibitor candidate in the test reaction mix relative to the control reaction mix. In specific embodiments, the steps of (B) and (G) are conducted for about 15 min, 30 min, 45 min, 60 min, 75 min, or 90 min. In some embodiments, the steps of (B) and (G) are conducted for about 45 min. In certain embodiments, the step of (E) is performed after a period of time of the step of (d) that results in a decrease in interfering short-lived background signals, and the step of (J) is performed after the same period of time of the step of (I). In certain embodiments, the steps of (A)-(E) are carried out for each Factor D inhibitor candidate from the plurality.

[0450] In certain embodiments when anti-Factor C3b antibody and anti-Factor Ba antibody are used, the anti-Factor C3b antibody is biotinylated, and the first moiety comprises streptavidin, avidin, or neutravidin. In some embodiments, the anti-Factor C3b antibody is biotinylated, and the first moiety comprises streptavidin. In certain embodiments, the anti-Factor Ba antibody is biotinylated, and the second moiety comprises streptavidin, avidin, or neutravidin. In some embodiments, the anti-Factor Ba antibody is biotinylated, and the second moiety comprises streptavidin.

[0451] In certain embodiments when anti-Factor C3b antibody and anti-Factor Ba antibody are used, the anti-Factor C3b antibody and the anti-Factor Ba antibody used in the methods of screening for a Factor D inhibitor quench the activity of Factor D. In such embodiments, the need to add another quencher specifically is obviated. In certain embodiments when anti-Factor C3b antibody and anti-Factor Ba antibody are used, the methods of screening for a Factor D inhibitor further comprise a step of quenching the activity of Factor D in the sample by providing an excessive amount of a quencher to the sample before the step of (c). When a control sample is used, in certain embodiments, the methods of screening for a Factor D inhibitor further comprise a step of quenching the activity of Factor D in the sample by providing an excessive amount of a quencher to the sample before the step of (c), and a step of quenching the activity of Factor D in the control sample by providing an excessive amount of the quencher to the control sample before the step of (g). In specific embodiments, the quencher is a Factor D inhibitor (for example, an anti-Factor D antibody or an excess amount of EDTA).

[0452] The control reaction mix can comprise, for example, a different Factor D inhibitor with known potency (e.g., 100% potency) or no Factor D inhibitor, but contains everything else essentially the same as the test reaction mix. In specific embodiments, more than one control reaction mix is used in the methods described herein. In certain embodiments, a standard curve has been generated for screening for Factor D inhibitors without the need to measure a control reaction mix.

[0453] The donor/acceptor pair can be any known in the art, or as described in Section 5.1.

[0454] The Factor D inhibitor candidate can be any pharmaceutical agent that may reduce or block the activity of Factor D. In specific embodiments, the Factor D inhibitor candidate is an antibody or an antigen-binding fragment thereof, for example, an antibody or an antigen-binding fragment thereof that binds to Factor D. In specific embodiments, the antibody is a bispecific antibody. In specific embodiments, the Factor D inhibitor candidate is a small molecule inhibitor. In specific embodiments, the Factor D inhibitor candidate is a nucleotide (e.g., a DNA, an RNA, an shRNA, an miRNA, an siRNA, an antisense DNA). In specific embodiments, the Factor D inhibitor candidate is a peptide, a protein, a peptide mimetic, an aptamer, or any other molecule that binds to Factor D.

[0455] In the methods of screening for a Factor D inhibitor described above, the anti-Factor Ba, anti-Factor Bb, and/or anti-Factor C3b may be replaced by a peptide, a non-antibody protein, a peptide mimetic, an aptamer, a nucleotide (e.g., DNA, RNA, shRNA, miRNA, siRNA, antisense DNA), or any other molecule that binds to Factor Ba, Factor Bb, or anti-Factor C3b, respectively. Alternatively, the Factor Ba, Factor Bb, and/or Factor C3b may be directed attached to the donor or acceptor (as the case may be) by direct chemical labeling.

[0456] In specific embodiments of the methods of screening for a Factor D inhibitor described herein, the Factor D is a recombinantly expressed Factor D. In specific embodiments of the methods of screening for a Factor D inhibitor described herein, the Factor D is endogenously expressed Factor D purified from a sample derived from a subject.

[0457] In specific embodiments of the methods of screening for a Factor D inhibitor described herein, the Factor B is a recombinantly expressed Factor B. In specific embodiments of the methods of screening for a Factor D inhibitor described herein, the Factor B is endogenously expressed Factor B purified from a sample derived from a subject.

[0458] The term "sample" referred to in the methods described herein, can be, but is not limited to, a blood sample or a serum sample.

[0459] The subject referred to in the methods described herein, can be, but is not limited to, a human or non-human vertebrate such as a wild, domestic or farm animal. In certain embodiments, the subject is a mammal, e.g., a human, a cow, a dog, a cat, a goat, a horse, a sheep, a pig, a rat, or a mouse. In a preferred embodiment, the subject is a human.

5.6. Kits

[0460] In another aspect, provided herein are kits for measuring Factor D activity, determining Factor D inhibitor potency, and/or screening for Factor D inhibitors. The kits described herein can be used in accordance with any methods described above as appropriate.

[0461] In various embodiments, the kits comprise an anti-Factor Ba antibody, an anti-Factor Bb antibody, a first moiety and a second moiety, wherein: (a) the anti-Factor Ba antibody is labeled or can be labeled with the first moiety, the anti-Factor Bb antibody is labeled or can be labeled with the second moiety; and (b) one of the moieties is a donor, and the other moiety is an acceptor. When using the kits, in specific embodiments a proximity signal can be generated by the donor and/or the acceptor, which indicates that the acceptor and the donor are in proximity.

[0462] When the proximity signal generated by the donor and/or the acceptor is based on energy transfer between the donor and the acceptor upon light activation, in various embodiments, the kits comprise an anti-Factor Ba antibody, an anti-Factor Bb antibody, a first moiety and a second moiety, wherein: (a) the anti-Factor Ba antibody is labeled or can be labeled with the first moiety, the anti-Factor Bb antibody is labeled or can be labeled with the second moiety; and (b) one of the moieties is a donor, and the other moiety is an acceptor. When using the kits, in specific embodiments upon excitation by a light source the ratio between the acceptor fluorescence emission intensity and the donor fluorescence emission intensity that is higher than a baseline level indicates that the donor and the acceptor are in proximity (a baseline level here is the ratio between the acceptor's fluorescence emission intensity and the donor's fluorescence emission intensity when the acceptor and the donor are apart (e.g., more than 10 nm, 20 nm, 50 nm, 100 nm, or 200 nm apart)).

[0463] In specific embodiments, the anti-Factor Ba antibody is biotinylated, and the first moiety comprises streptavidin, avidin, or neutravidin. In some embodiments, the anti-Factor Ba antibody is biotinylated, and the first moiety comprises streptavidin. In certain embodiments, the anti-Factor Bb antibody is biotinylated, and the second moiety comprises streptavidin, avidin, or neutravidin. In some embodiments, the anti-Factor Bb antibody is biotinylated, and the second moiety comprises streptavidin.

[0464] In specific embodiments, the anti-Factor Ba antibody and/or the anti-Factor Bb antibody is immobilized on a solid surface. In specific embodiments, the solid surface is a plate, a microplate, a chip, a membrane, or a bead.

[0465] In other various embodiments, the kits comprise an anti-Factor C3b antibody, an anti-Factor Ba antibody, a first moiety and a second moiety, wherein: (a) the anti-Factor C3b antibody is labeled or can be labeled with the first moiety, the anti-Factor Ba antibody is labeled or can be labeled with the second moiety; and (b) one of the moieties is a donor, and the other moiety is an acceptor. When using the kits, in specific embodiments a proximity signal can be generated by the donor and/or the acceptor, which indicates that the acceptor and the donor are in proximity.

[0466] When the proximity signal generated by the donor and/or the acceptor is based on energy transfer between the donor and the acceptor upon light activation, in various embodiments, the kits comprise an anti-Factor C3b antibody, an anti-Factor Ba antibody, a first moiety and a second moiety, wherein: (a) the anti-Factor C3b antibody is labeled or can be labeled with the first moiety, the anti-Factor Ba antibody is labeled or can be labeled with the second moiety; and (b) one of the moieties is a donor, and the other moiety is an acceptor. When using the kits, in specific embodiments upon excitation by a light source the ratio between the acceptor fluorescence emission intensity and the donor fluorescence emission intensity that is higher than a baseline level indicates that the donor and the acceptor are in proximity (a baseline level here is the ratio between the acceptor's fluorescence emission intensity and the donor's fluorescence emission intensity when the acceptor and the donor are apart (e.g., more than 10 nm, 20 nm, 50 nm, 100 nm, or 200 nm apart)).

[0467] In specific embodiments, the anti-Factor C3b antibody is biotinylated, and the first moiety comprises streptavidin, avidin, or neutravidin. In some embodiments, the anti-Factor C3b antibody is biotinylated, and the first moiety comprises streptavidin. In certain embodiments, the anti-Factor Ba antibody is biotinylated, and the second moiety comprises streptavidin, avidin, or neutravidin. In some embodiments, the anti-Factor Ba antibody is biotinylated, and the second moiety comprises streptavidin.

[0468] In specific embodiments, the anti-Factor C3b antibody and/or the anti-Factor Ba antibody is immobilized on a solid surface. In specific embodiments, the solid surface is a plate, a microplate, a chip, a membrane, or a bead.

[0469] In certain embodiments, the kits described herein further comprise a control sample with known Factor D activity.

[0470] In certain embodiments, the kits described herein further comprise a control Factor D inhibitor with known potency of inhibiting Factor D activity (e.g., 100% potency). In certain embodiments, the kits further comprise a control sample containing no Factor D inhibitor.

[0471] In certain embodiments, the kits described herein further comprise a quencher. In specific embodiments, the quencher is a Factor D inhibitor (for example, an anti-Factor D antibody or an excess amount of EDTA).

[0472] In specific embodiments, the kits further comprise a recombinantly expressed Factor B. In specific embodiments, the kits further comprise an endogenously expressed Factor B purified from a sample derived from a subject.

[0473] In specific embodiments, the kits further comprise a recombinantly expressed Factor D. In specific embodiments,

the kits further comprise an endogenously expressed Factor D purified from a sample derived from a subject.

[0474] The term "sample" referred to in the kits described herein, can be, but is not limited to, a blood sample or a serum sample.

[0475] The subject referred to in the kits described herein, can be, but is not limited to, a human or non-human vertebrate such as a wild, domestic or farm animal. In certain embodiments, the subject is a mammal, e.g., a human, a cow, a dog, a cat, a goat, a horse, a sheep, a pig, a rat, or a mouse. In a preferred embodiment, the subject is a human.

[0476] The donor/acceptor pair can be any known in the art, or as described in Section 5.1

[0477] The individual components of the kits (e.g., anti-Factor Ba antibody, anti-Factor Bb antibody, first moiety, second moiety, quencher, control) can be packed in one or more containers. In some embodiments, each component is packed in its own container. In some embodiments when the kit comprises anti-Factor Ba antibody and anti-Factor Bb antibody, anti-Factor Ba antibody and the first moiety are packed in one container. In some embodiments when the kit comprises anti-Factor Ba antibody and anti-Factor Bb antibody, anti-Factor Bb antibody and the second moiety are packed in one container. In some embodiments when the kit comprises anti-Factor C3b antibody and anti-Factor Ba antibody, anti-Factor C3b antibody and the first moiety are packed in one container. In some embodiments when the kit comprises anti-Factor C3b antibody and anti-Factor Ba antibody, anti-Factor Ba antibody and the second moiety are packed in one container. The one or more containers can comprise bottle(s), vial(s), tube(s), plate(s), and/or microplate(s). In specific embodiments, the kits further comprise instructions for use of the kits.

6. EXAMPLE

[0478] This following non-limiting example demonstrates that proximity-based measurement assays are desirable methods to measure Factor D activity and Factor D inhibitor potency.

6.1. Introduction

[0479] Factor D activity has been identified as the key driver in the activation of the alternative complement pathway.

[0480] Lampalizumab is a Fab directed against the complement component Factor D (Katsche et al., 2012, J Biol Chem 287:12886-12892). Factor D is a highly specific chymotrypsin-like serine protease that is a rate-limiting enzyme in the activation of the complement alternative pathway (Katsche et al., 2012, J Biol Chem 287:12886-12892). The substrate for Factor D is another alternative complement pathway serine protease, Factor B. Factor C3b binds to Factor B; then, Factor D cleaves Factor B into Factor Ba and Factor Bb (Volanakis and Narayana, 1996, Protein Sci 5:553-564). Factor Bb remains bound to Factor C3b, forming the active C3 convertase, which initiates the alternative complement pathway. Increased activation of the alternative complement pathway has been found in drusen, cytotoxic deposits present on the Bruch's membrane, which are associated with the development of age-related macular degeneration (AMD) (Damico et al., 2012, Arq Bras Oftalmol 75:71-75).

[0481] Lampalizumab inhibits Factor D-mediated cleavage of Factor B, preventing alternative pathway activation, and thereby inhibiting inflammation and cytotoxic activity of the activated complement components (Tanhehco, 1999, Transplant Proc 31:2168-2171).

[0482] Activation of the alternative complement pathway is typically measured by adding human serum to rabbit erythrocytes. Next, intact erythrocytes and cellular debris are pelleted by centrifugation and lysis is determined by measuring the absorbance at 412 nm arising from the release of hemoglobin into the supernatant.

[0483] An alternative method was developed to measure Factor D enzymatic activity by measuring the cleavage of Factor B using Time Resolved-Forster Energy Resonance Transfer (*i.e.*, fluorescence resonance energy transfer, FRET). The method was used to characterize the activity of a neutralizing Fab fragment directed against Factor D. This assay is simple, homogeneous and shows reproducible dose-response curves in the concentration range of 2 to 125 ng/mL. With interassay variability of less than 5% and recovery of 97-104%, this assay demonstrates acceptable precision and accuracy, and it is able to detect degradative changes in the anti-Factor D Fab fragment samples subjected to oxidative stress, suggesting that it is suitable for use as a potency method in quality control.

[0484] Strategies for assay development and optimization, as well as results from the characterization of the assay are presented below.

6.2. Materials and Methods

6.2.1. Materials

[0485] The following reagents were used for the FRET study: Lampalizumab, recombinant human Factor D and the anti-Factor Ba and anti-Factor Bb antibodies were generated at Genentech (South San Francisco, CA). Complement Factor B and Complement Factor C3b were purchased from Complement Technologies (Tyler, TX). Biotinylation of anti-

Factor Bb was performed at Genentech using a kit purchased from Pierce (Rockland, IL). The Streptavidin-Alexa Fluor 647 and custom conjugation of Complement Factor Ba to Europium were provided by Life Technologies (Grand Island, NY).

[0486] The following reagents were used for the AlphaScreen assay: the anti-Factor B antibodies, Complement Factors B, Factor C3b and Factor D, and the anti-Factor D antibody are as described above. The Streptavidin-coated donor beads and acceptor beads were purchased from Perkin Elmer (Waltham, Massachusetts).

[0487] The following reagents were used for the hemolysis assay: rabbit erythrocytes were purchased from Colorado Serum (Denver, CO). Veronal buffer and Gelatin were purchased from Lonza (Allendale, NJ). Clq-depleted human serum was purchased from Quidel (San Diego, CA).

6.2.2. Factor B Cleavage Assay Procedure

[0488] Figure 1 shows the assay schematic for the Lampalizumab TR-FRET (Time Resolved-FRET) assay. All reagents were prepared in Enzymatic Reaction Buffer (75 mM Sodium Chloride 1 mM Magnesium Chloride, 25 mM Tris, 0.005% Tween 20 pH 7.3). Reference and sample Lampalizumab were titrated. Factor D was diluted to 12.5 ng/mL and Lampalizumab titrations were added 1:1 with the diluted Factor D. Complement Factor B and Complement Factor C3b were diluted to 1 µg/mL and 7 µg/mL, respectively, and combined 1:1. 50 µL per well of the Lampalizumab/Factor D mixture was added to a non-binding 96 well plate from Greiner (Monroe, NC) followed by 50 µL of the Factor B/Factor C3b mixture and the plate was incubated for 45 minutes with gentle agitation at 25°C. Working concentrations of these reagents were determined by AlphaScreen (data not shown). 50 µL of the detection mixture (1.2 µg/mL biotinylated anti-Factor Bb, 4.0 nM anti-Factor Ba-Europium and 25 nM Streptavidin-Alexa Fluor 647) was added and the plate was incubated for 1 hour with gentle agitation at 25°C. The Europium and Alexa Fluor 647 fluorescence signals were measured on a Paradigm plate reader with an HTRF cartridge (Molecular Devices Sunnyvale, CA) with filters appropriate for the excitation of Europium (340 nm) and emission of the Europium and Alexa 647 fluorophores (615 nm and 665 nm, respectively). The TR-FRET ratio was determined by dividing the fluorescence from the Alexa 647 by the fluorescence of the Europium and multiplying by 10,000. The TR-FRET ratio of the Lampalizumab was plotted against the antibody concentrations using a 4 parameter curve-fitting program (Softmax Pro, Molecular Devices, Sunnyvale, CA).

6.2.3. Hemolysis Assay Procedure

[0489] For determining alternative pathway activity, rabbit erythrocytes (Er) were washed 3 times in Gelatin Veronal Buffer (GVB) (0.1% gelatin in veronal buffer and resuspended to 2 x 10⁹/ml). Lampalizumab (50 µl) and 20 µl of Er suspension were mixed 1:1 with GVB/0.1M EGTA/0.1M MgCl₂. Complement activation was initiated by the addition of C1q-depleted human serum (Quidel; 30 µl diluted 1:3 in GVB). After a 30 minute incubation at room temperature, 200 µl GVB/10 mM EDTA were added to stop the reaction and samples were centrifuged for 5 min at 500 g. Hemolysis was quantified in 200 µl supernatant by measuring absorbance at 412 nm. Data were expressed as % of hemolysis induced in the absence of the inhibitor.

6.3. Results

6.3.1. Optimization of Conditions for Detection of Factor B Cleavage

[0490] In order to optimize the signal of the TR-FRET assay, varying concentrations of the Streptavidin-Alexa-Fluor 647 and anti-Factor Ba-Europium were analyzed with fixed concentrations of the other reagents and then the assay was performed as described in Section 6.1. Figure 2 shows this co-titration of Streptavidin-Alexa-Fluor 647 and anti-Factor Ba-Europium. Working concentrations of the Streptavidin-Alexa-Fluor 647 and anti-Factor Ba-Europium that provided optimal signal were 4.0 nM anti-Factor Ba-Europium and 25 nM Streptavidin-Alexa Fluor 647, respectively.

[0491] The anti-Factor Ba and anti-Factor Bb detection reagents were tested for their ability to inhibit the cleavage of Factor B by Factor D. Figure 3 shows that the activity of Factor D was greatly diminished when the detection reagents were added from prior to initiation of the enzymatic reaction (t=0) and increased with increasing time. The small amount of activity seen in the t=0 is likely due to incomplete inactivation of Factor D by anti-Factor Ba and anti-Factor Bb and the extended amount of time required to conduct this experiment. The forty-five minute enzymatic incubation time was determined to provide suitable signal and robust method performance.

[0492] Next, the incubation with detection reagents was optimized. The assay was run as described in Section 6.2, but the incubation with detection reagent was varied from 10 - 120 minutes. As seen in Figure 4, a 60 minute detection reagent incubation provided suitable signal and robust method performance.

[0493] To demonstrate that it is possible to use alternate detection reagents to measure cleavage of Factor B, the assay was performed using AlphaScreen reagents. Streptavidin-conjugated alpha donor beads and anti-Factor Ba-

conjugated alpha acceptor beads were substituted for TR-FRET reagent. Figures 5A and 5B show that both detection technologies generated good signal and dynamic range.

6.3.2. Characterization of the anti-Factor D TR-FRET assay

[0494] Using the final assay format, we further characterized the assay by conducting a study for initial evaluation of accuracy and precision. Briefly, anti-Factor D was diluted to nominal concentrations of 0.3, 0.4, 0.5, 0.6 and 0.7 mg/mL, corresponding to 60, 80, 100 and 120 and 140% of the target concentration of 0.5 mg/mL, respectively. The protein concentrations of these dilutions were determined accurately by a UV spectrophotometric scan and determined to be 0.307, 0.381, 0.512, 0.597, 0.722 mg/mL. Each sample was subsequently diluted further into Enzymatic Reaction buffer and tested as described in Section 6.1. Each sample was assayed twelve times (6 times each by 2 different analysts) using new sample and reference dilutions for each assay.

[0495] To assess the accuracy of the assay, the measured activities were divided by the expected activities and expressed as percentage recoveries. Table 10 shows that mean activities of 60, 79, 100, 120 and 139% were obtained. This represents percentage recoveries ranging from 97-104%. Interassay variability, indicated by coefficient of variation (CV) was less than 5%.

[0496] These data strongly suggest that the assay is sensitive to differences in affinity

Table 10. Assessment of the accuracy of the Lampalizumab TR-FRET assay

Expected activity (mg/mL)	Measure Activity (mg/mL) Mean +/- SD (n =12)	Accuracy %	Interassay CV %
0.307	0.300 +/- 0.0102	98	3
0.381	0.395 +/- 0.0096	104	3
0.512	0.500 +/- 0.0154	98	3
0.597	0.600 +/- 0.0259	101	5
0.722	0.695 +/- 0.0260	97	4

[0497] The ability of the Factor B cleavage assay to detect changes in activity of Lampalizumab samples subjected to stress was evaluated. Each sample was tested in 3 assays according to the method described above. The results are summarized in Table 11. Lampalizumab samples subjected to oxidation conditions (30 mM AAPH) exhibited a reduced activity of 63% compared to the control value of 93%.

Table 11. Assessment of the ability of the Lampalizumab TR-FRET assay to detect changes in activity of samples subjected to oxidation stress

Stressed Sample	TR-FRET Activity	Hemolytic Mean
Unstressed control	93 +/- 9	81 +/- 27
Oxidized, 30mM AAPH	63 +/- 6	82 +/- 16
Thermal Stress	86 (1% diff)	102 +/- 23
Thermal control	103 (0 % diff)	96 +/- 18

[0498] The activity of the stress samples was also measured using the rabbit erythrocyte lysis assay to compare the capability of the two methods. The data from this comparison are shown in Table 11 and demonstrate that the Factor B cleavage method is more precise and more sensitive to thermal and oxidative degradation.

6.4. Conclusion

[0499] The activity of Lampalizumab is dependent on its ability to bind to Factor D and inhibit its enzymatic activity. This type of activity can be measured *in vitro* by monitoring rabbit erythrocyte cell lysis after incubation with the Fab fragment. The TR-FRET assay described here measures the ability of Lampalizumab to bind to and inhibit the enzymatic activity of Factor D, the rate-limiting step in activation of the Alternate Complement pathway. To determine whether this method could serve as a suitable measure of Factor D activity, it was assessed for its ability to detect changes in the activity of Lampalizumab that was subjected to oxidative stress, and the data generated by this method were compared to data generated with a more established hemolytic method. The TR-FRET assay is capable of detecting losses in the activity of anti-Factor D subjected to oxidative stress. The results obtained using the TR-FRET assay reveal more

sensitivity to stress than the hemolytic method, demonstrating that the TR-FRET assay is a suitable method to measure Factor D activity.

7. Incorporation by reference

[0500] Various references such as patents, patent applications, and publications are cited herein, the disclosures of which are hereby incorporated by reference herein in their entireties.

[0501] The following numbered clauses, describing aspects of the invention, are part of the description:

1. A method of measuring the activity of Factor D in a sample derived from a subject, comprising performing a proximity-based measurement assay, wherein the proximity-based measurement assay measures the cleavage of Factor B.

2. The method of clause 1, comprising:

(a) adding to the sample an anti-Factor Ba antibody labeled with a first moiety and an anti-Factor Bb antibody labeled with a second moiety, wherein one of the moieties is a donor, and the other moiety is an acceptor, and wherein a proximity signal generated by the acceptor and/or the donor indicates that Factor Ba and Factor Bb are in proximity; and

(b) measuring the value of the proximity signal from the sample;

wherein the activity of Factor D in the sample is negatively correlated with the value of the proximity signal.

3. The method of clause 2, further comprising:

(c) adding to a control sample the anti-Factor Ba antibody labeled with the first moiety and the anti-Factor Bb antibody labeled with the second moiety; and

(d) measuring the value of the proximity signal from the control sample;

wherein a greater value of the proximity signal from the sample relative to the control sample indicates a lower activity of Factor D in the sample relative to the control sample.

4. The method of clause 2 or 3, wherein the anti-Factor Ba antibody and the anti-Factor Bb antibody quench the activity of Factor D.

5. The method of clause 1, comprising:

(a) adding to the sample an anti-Factor C3b antibody labeled with a first moiety and an anti-Factor Ba antibody labeled with a second moiety, wherein one of the moieties is a donor, and the other moiety is an acceptor, and wherein a proximity signal generated by the acceptor and/or the donor indicates that Factor C3b and Factor Ba are in proximity; and

(b) measuring the value of the proximity signal from the sample;

wherein the activity of Factor D in the sample is negatively correlated with the value of the proximity signal.

6. The method of clause 5, further comprising:

(c) adding to a control sample the anti-Factor C3b antibody labeled with the first moiety and the anti-Factor Ba antibody labeled with the second moiety; and

(d) measuring the value of the proximity signal from the control sample;

wherein a greater value of the proximity signal from the sample relative to the control sample indicates a lower activity of Factor D in the sample relative to the control sample.

7. The method of clause 2 or 5, further comprising a step of quenching the activity of Factor D in the sample by providing an excessive amount of a quencher to the sample before the step of (a).

8. The method of clause 3 or 6, further comprising a step of quenching the activity of Factor D in the sample by providing an excessive amount of a quencher to the sample before the step of (a), and a step of quenching the activity of Factor D in the control sample by providing an excessive amount of the quencher to the control sample before the step of (c).

9. The method of clause 7 or 8, wherein the quencher is a Factor D inhibitor.

10. The method of any of clauses 1-9, wherein the subject is a human.

11. A method of determining the potency of a Factor D inhibitor in inhibiting Factor D activity, comprising performing a proximity-based measurement assay, wherein the proximity-based measurement assay measures the cleavage of Factor B.

12. The method of clause 11, comprising:

- (a) mixing the Factor D inhibitor with Factor D, Factor B and Factor C3b in a test reaction mix;
- (b) incubating the test reaction mix;
- (c) adding to the test reaction mix an anti-Factor Ba antibody labeled with a first moiety and an anti-Factor Bb antibody labeled with a second moiety after the step of (b), wherein one of the moieties is a donor, and the other moiety is an acceptor, and wherein a proximity signal generated by the acceptor and/or the donor indicates that Factor Ba and Factor Bb are in proximity; and
- (d) measuring the value of the proximity signal from the test reaction mix;

wherein the potency of the Factor D inhibitor is positively correlated with the value of the proximity signal.

13. The method of clause 12, further comprising:

- (e) mixing a control reaction mix;
- (f) incubating the control reaction mix;
- (g) adding to the control reaction mix the anti-Factor Ba antibody labeled with the first moiety and the anti-Factor Bb antibody labeled with the second moiety after the step of (f); and
- (h) measuring the value of the proximity signal from the control test reaction mix;

wherein a greater value of the proximity signal from the test reaction mix relative to the control reaction mix indicates a greater inhibition of Factor D activity by the Factor D inhibitor in the test reaction mix relative to the control reaction mix.

14. The method of clause 12 or 13, wherein the anti-Factor Ba antibody and the anti-Factor Bb antibody quench the activity of Factor D.

15. The method of clause 11, comprising:

- (a) mixing the Factor D inhibitor with Factor D, Factor B and Factor C3b in a test reaction mix;
- (b) incubating the test reaction mix;
- (c) adding to the test reaction mix an anti-Factor C3b antibody labeled with a first moiety and an anti-Factor Ba antibody labeled with a second moiety after the step of (b), wherein one of the moieties is a donor, and the other moiety is an acceptor, and wherein a proximity signal generated by the acceptor and/or the donor indicates that Factor C3b and Factor Ba are in proximity; and
- (d) measuring the value of the proximity signal from the test reaction mix;

wherein the potency of the Factor D inhibitor is positively correlated with the value of the proximity signal.

16. The method of clause 15, further comprising:

- (e) mixing a control reaction mix;
- (f) incubating the control reaction mix;
- (g) adding to the control reaction mix the anti-Factor C3b antibody labeled with the first moiety and the anti-Factor Ba antibody labeled with the second moiety after the step of (f); and
- (h) measuring the value of the proximity signal from the control test reaction mix;

wherein a greater value of the proximity signal from the test reaction mix relative to the control reaction mix indicates a greater inhibition of Factor D activity by the Factor D inhibitor in the test reaction mix relative to the control reaction mix.

17. The method of clause 12 or 15, further comprising a step of quenching the activity of Factor D in the sample by providing an excessive amount of a quencher to the sample before the step of (c).

18. The method of clause 13 or 16, further comprising a step of quenching the activity of Factor D in the sample by providing an excessive amount of a quencher to the sample before the step of (c), and a step of quenching the activity of Factor D in the control sample by providing an excessive amount of the quencher to the control sample before the step of (h).

19. The method of clause 17 or 18, wherein the quencher is a Factor D inhibitor.

20. The method of any of clauses 11-19, wherein the Factor D inhibitor is an antibody or an antigen-binding fragment thereof.

21. The method of clause 20, wherein the antibody is lampalizumab.

22. The method of clause 20, wherein the antibody comprises one, two, three, four, five or six of the following HVRs: (i) an HVR-H1 comprising the amino acid sequence of SEQ ID NO: 1; (ii) an HVR-H2 comprising the amino acid sequence of SEQ ID NO: 2, SEQ ID NO: 3, or SEQ ID NO: 4; (iii) an HVR-H3 comprising the amino acid sequence of SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, or SEQ ID NO: 8; (iv) an HVR-L1 comprising the amino acid sequence of SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, or SEQ ID NO: 17; (v) an HVR-L2 comprising the amino acid sequence of SEQ ID NO: 18; or (vi) an HVR-L3 comprising the amino acid sequence of SEQ ID NO: 19 or SEQ ID NO: 20.

23. The method of clause 20, wherein the antibody comprises one, two, three, four, five or six of the following HVRs: (i) an HVR-H1 comprising the amino acid sequence of SEQ ID NO: 85; (ii) an HVR-H2 comprising the amino acid sequence of SEQ ID NO: 86, SEQ ID NO: 87, SEQ ID NO: 88, SEQ ID NO: 89, SEQ ID NO: 90, SEQ ID NO: 91, SEQ ID NO: 92, SEQ ID NO: 93, or SEQ ID NO: 94; (iii) an HVR-H3 comprising the amino acid sequence of SEQ ID NO: 95; (iv) an HVR-L1 comprising the amino acid sequence of SEQ ID NO: 96; (v) an HVR-L2 comprising the amino acid sequence of SEQ ID NO: 97, SEQ ID NO: 98, or SEQ ID NO: 99; or (vi) an HVR-L3 comprising the amino acid sequence of SEQ ID NO: 100 or SEQ ID NO: 101.

24. A method of screening for a Factor D inhibitor from a plurality of Factor D inhibitor candidates, comprising performing a proximity-based measurement assay, wherein the proximity-based measurement assay measures the cleavage of Factor B.

25. The method of clause 24, comprising:

- (a) mixing a Factor D inhibitor candidate with Factor D, Factor B and Factor C3b in a test reaction mix;
- (b) incubating the test reaction mix;
- (c) adding to the test reaction mix an anti-Factor Ba antibody labeled with a first moiety and an anti-Factor Bb antibody labeled with a second moiety after the step of (b), wherein one of the moieties is a donor, and the other is an acceptor, and wherein a proximity signal generated by the acceptor and/or the donor indicates that Factor Ba and Factor Bb are in proximity; and
- (d) measuring the value of the proximity signal from the test reaction mix;

wherein the degree of Factor D activity inhibition by a Factor D candidate is positively correlated with the value of the proximity signal.

26. The method of clause 25, further comprising:

- (e) mixing a control reaction mix;
- (f) incubating the control reaction mix;
- (g) adding to the control reaction mix the anti-Factor Ba antibody labeled with the first moiety and the anti-Factor Bb antibody labeled with the second moiety after the step of (g); and
- (h) measuring the value of the proximity signal from the control test reaction mix; wherein a greater value of the proximity signal from the test reaction mix relative to the control reaction mix indicates a greater inhibition of Factor D activity by the Factor D inhibitor candidate in the test reaction mix relative to the control reaction mix.

27. The method of clause 25 or 26, wherein the anti-Factor Ba antibody and the anti-Factor Bb antibody quench the activity of Factor D.

28. The method of clause 24, comprising:

- (a) mixing a Factor D inhibitor candidate with Factor D, Factor B and Factor C3b in a test reaction mix;
- (b) incubating the test reaction mix;
- (c) adding to the test reaction mix an anti-Factor C3b antibody labeled with a first moiety and an anti-Factor Ba antibody labeled with a second moiety after the step of (b), wherein one of the moieties is a donor, and the other is an acceptor, and wherein a proximity signal generated by the acceptor and/or the donor indicates that Factor C3b and Factor Ba are in proximity; and
- (d) measuring the value of the proximity signal from the test reaction mix;

wherein the degree of Factor D activity inhibition by a Factor D candidate is positively correlated with the value of the proximity signal.

29. The method of clause 28, further comprising:

- (e) mixing a control reaction mix;
- (f) incubating the control reaction mix;

- (g) adding to the control reaction mix the anti-Factor C3b antibody labeled with the first moiety and the anti-Factor Ba antibody labeled with the second moiety after the step of (g); and
- (h) measuring the value of the proximity signal from the control test reaction mix;

wherein a greater value of the proximity signal from the test reaction mix relative to the control reaction mix indicates a greater inhibition of Factor D activity by the Factor D inhibitor candidate in the test reaction mix relative to the control reaction mix.

30. The method of clause 25 or 28, further comprising a step of quenching the activity of Factor D in the sample by providing an excessive amount of a quencher to the sample before the step of (c).

31. The method of clause 26 or 29, further comprising a step of quenching the activity of Factor D in the sample by providing an excessive amount of a quencher to the sample before the step of (c), and a step of quenching the activity of Factor D in the control sample by providing an excessive amount of the quencher to the control sample before the step of (g).

32. The method of clause 30 or 31, wherein the quencher is a Factor D inhibitor.

33. The method of any of clauses 25-32, wherein the steps of (a)-(d) are carried out for each Factor D inhibitor candidate from the plurality.

34. The method of any of clauses 24-33, wherein the Factor D inhibitor candidate is an antibody or an antigen-binding fragment thereof.

35. The method of any of clauses 12-23 and 25-34, wherein the Factor D is a recombinantly expressed Factor D.

36. The method of any of clauses 12-23 and 25-34, wherein the Factor D is endogenously expressed Factor D purified from a sample derived from a subject.

37. The method of any of clauses 1-36, wherein the Factor B is a recombinantly expressed Factor B.

38. The method of any of clauses 1-36, wherein the Factor B is endogenously expressed Factor B purified from a sample derived from a subject.

39. A kit comprising an anti-Factor Ba antibody, an anti-Factor Bb antibody, a first moiety and a second moiety, wherein:

(a) the anti-Factor Ba antibody is labeled or can be labeled with the first moiety, the anti-Factor Bb antibody is labeled or can be labeled with the second moiety; and

(b) one of the moieties is a donor, and the other moiety is an acceptor.

40. The kit of clause 39, wherein the anti-Factor Ba antibody and/or the anti-Factor Bb antibody is immobilized on a solid surface.

41. A kit comprising an anti-Factor C3b antibody, an anti-Factor Ba antibody, a first moiety and a second moiety, wherein:

(a) the anti-Factor C3b antibody is labeled or can be labeled with the first moiety, the anti-Factor Ba antibody is labeled or can be labeled with the second moiety; and

(b) one of the moieties is a donor, and the other moiety is an acceptor.

42. The kit of clause 41, wherein the anti-Factor C3b antibody and/or the anti-Factor Ba antibody is immobilized on a solid surface.

43. The kit of clause 40 or 42, wherein the solid surface is a plate, a microplate, a chip, a membrane, or a bead.

44. The kit of any of clauses 39-43, further comprising a control sample with known Factor D activity.

45. The kit of any of clauses 39-43, further comprising a control Factor D inhibitor with known potency of inhibiting Factor D activity.

46. The kit of any of clauses 39-45, further comprising a quencher.

47. The kit of clause 46, wherein the quencher is a Factor D inhibitor.

48. The kit of any of clauses 39-47, further comprising a recombinantly expressed Factor B.

49. The kit of any of clauses 39-47, further comprising an endogenously expressed Factor B purified from a sample derived from a subject.

50. The kit of any of clauses 39-49, further comprising a recombinantly expressed Factor D.

51. The kit of any of clauses 39-49, further comprising an endogenously expressed Factor D purified from a sample derived from a subject.

Claims

1. A method of measuring the activity of Factor D in a sample derived from a subject, comprising performing a proximity-based measurement assay, wherein the proximity-based measurement assay measures the cleavage of Factor B, the method comprising:

(a) adding to the sample an anti-Factor C3b antibody labeled with a first moiety and an anti-Factor Ba antibody labeled with a second moiety, wherein one of the moieties is a donor, and the other moiety is an acceptor, and wherein a proximity signal generated by the acceptor and/or the donor indicates that Factor C3b and Factor Ba are in proximity; and
(b) measuring the value of the proximity signal from the sample;

wherein the activity of Factor D in the sample is negatively correlated with the value of the proximity signal.

2. The method of claim 1, further comprising:

(c) adding to a control sample the anti-Factor C3b antibody labeled with the first moiety and the anti-Factor Ba antibody labeled with the second moiety; and
(d) measuring the value of the proximity signal from the control sample;

wherein a greater value of the proximity signal from the sample relative to the control sample indicates a lower activity of Factor D in the sample relative to the control sample.

3. The method of claim 1, further comprising a step of quenching the activity of Factor D in the sample by providing an excessive amount of a quencher to the sample before the step of (a), in particular wherein the quencher is a Factor D inhibitor.

4. The method of claim 2, further comprising a step of quenching the activity of Factor D in the sample by providing an excessive amount of a quencher to the sample before the step of (a), and a step of quenching the activity of Factor D in the control sample by providing an excessive amount of the quencher to the control sample before the step of (c), in particular wherein the quencher is a Factor D inhibitor.

5. The method of any of claims 1-4, wherein the subject is a human.

6. The method of claim 1 for determining the potency of a Factor D inhibitor in inhibiting Factor D activity, the method comprising:

(a) mixing the Factor D inhibitor with Factor D, Factor B and Factor C3b in a test reaction mix;
(b) incubating the test reaction mix;
(c) adding to the test reaction mix an anti-Factor C3b antibody labeled with a first moiety and an anti-Factor Ba antibody labeled with a second moiety after the step of (b), wherein one of the moieties is a donor, and the other moiety is an acceptor, and wherein a proximity signal generated by the acceptor and/or the donor indicates that Factor C3b and Factor Ba are in proximity; and
(d) measuring the value of the proximity signal from the test reaction mix;

wherein the potency of the Factor D inhibitor is positively correlated with the value of the proximity signal.

7. The method of claim 6, further comprising:

(e) mixing a control reaction mix;
(f) incubating the control reaction mix;
(g) adding to the control reaction mix the anti-Factor C3b antibody labeled with the first moiety and the anti-Factor Ba antibody labeled with the second moiety after the step of (f); and
(h) measuring the value of the proximity signal from the control test reaction mix;

wherein a greater value of the proximity signal from the test reaction mix relative to the control reaction mix indicates a greater inhibition of Factor D activity by the Factor D inhibitor in the test reaction mix relative to the control reaction mix.

8. The method of claim 6, further comprising a step of quenching the activity of Factor D in the sample by providing an excessive amount of a quencher to the sample before the step of (c), in particular wherein the quencher is a Factor D inhibitor.

9. The method of claim 7, further comprising a step of quenching the activity of Factor D in the sample by providing an excessive amount of a quencher to the sample before the step of (c), and a step of quenching the activity of Factor D in the control sample by providing an excessive amount of the quencher to the control sample before the step of (h), in particular wherein the quencher is a Factor D inhibitor.

10. The method of any of claims 6-9, wherein the Factor D inhibitor is an antibody or an antigen-binding fragment thereof.

11. The method of claim 10, wherein

(i) the antibody is lampalizumab,

(ii) the antibody comprises one, two, three, four, five or six of the following HVRs: (i) an HVR-H1 comprising the amino acid sequence of SEQ ID NO: 1; (ii) an HVR-H2 comprising the amino acid sequence of SEQ ID NO: 2, SEQ ID NO: 3, or SEQ ID NO: 4;

(iii) an HVR-H3 comprising the amino acid sequence of SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, or SEQ ID NO: 8; (iv) an HVR-L1 comprising the amino acid sequence of SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, or SEQ ID NO: 17; (v) an HVR-L2 comprising the amino acid sequence of SEQ ID NO: 18; or (vi) an HVR-L3 comprising the amino acid sequence of SEQ ID NO: 19 or SEQ ID NO: 20, or

(iii) the antibody comprises one, two, three, four, five or six of the following HVRs: (i) an HVR-H1 comprising the amino acid sequence of SEQ ID NO: 85; (ii) an HVR-H2 comprising the amino acid sequence of SEQ ID NO: 86, SEQ ID NO: 87, SEQ ID NO: 88, SEQ ID NO: 89, SEQ ID NO: 90, SEQ ID NO: 91, SEQ ID NO: 92, SEQ ID NO: 93, or SEQ ID NO: 94; (iii) an HVR-H3 comprising the amino acid sequence of SEQ ID NO: 95; (iv) an HVR-L1 comprising the amino acid sequence of SEQ ID NO: 96; (v) an HVR-L2 comprising the amino acid sequence of SEQ ID NO: 97, SEQ ID NO: 98, or SEQ ID NO: 99; or (vi) an HVR-L3 comprising the amino acid sequence of SEQ ID NO: 100 or SEQ ID NO: 101.

12. The method of claim 1 for screening for a Factor D inhibitor from a plurality of Factor D inhibitor candidates, the method comprising:

(a) mixing a Factor D inhibitor candidate with Factor D, Factor B and Factor C3b in a test reaction mix;

(b) incubating the test reaction mix;

(c) adding to the test reaction mix an anti-Factor C3b antibody labeled with a first moiety and an anti-Factor Ba antibody labeled with a second moiety after the step of (b), wherein one of the moieties is a donor, and the other is an acceptor, and wherein a proximity signal generated by the acceptor and/or the donor indicates that Factor C3b and Factor Ba are in proximity; and

(d) measuring the value of the proximity signal from the test reaction mix;

wherein the degree of Factor D activity inhibition by a Factor D candidate is positively correlated with the value of the proximity signal.

13. The method of claim 12, further comprising:

(e) mixing a control reaction mix;

(f) incubating the control reaction mix;

(g) adding to the control reaction mix the anti-Factor C3b antibody labeled with the first moiety and the anti-Factor Ba antibody labeled with the second moiety after the step of (g); and

(h) measuring the value of the proximity signal from the control test reaction mix;

wherein a greater value of the proximity signal from the test reaction mix relative to the control reaction mix indicates a greater inhibition of Factor D activity by the Factor D inhibitor candidate in the test reaction mix relative to the control reaction mix.

14. The method of claim 12, further comprising a step of quenching the activity of Factor D in the sample by providing an excessive amount of a quencher to the sample before the step of (c), in particular wherein the quencher is a

Factor D inhibitor.

- 5 15. The method of claim 14, further comprising a step of quenching the activity of Factor D in the sample by providing an excessive amount of a quencher to the sample before the step of (c), and a step of quenching the activity of Factor D in the control sample by providing an excessive amount of the quencher to the control sample before the step of (g), in particular wherein the quencher is a Factor D inhibitor.
- 10 16. The method of any of claims 12-15, wherein the steps of (a)-(d) are carried out for each Factor D inhibitor candidate from the plurality.
- 15 17. The method of any of claims 12-16, wherein the Factor D inhibitor candidate is an antibody or an antigen-binding fragment thereof.
18. The method of any of claims 6-17, wherein the Factor D is (i) a recombinantly expressed Factor D, or (ii) endogenously expressed Factor D purified from a sample derived from a subject.
19. The method of any of claims 1-18, wherein the Factor B is (i) a recombinantly expressed Factor B, or (ii) endogenously expressed Factor B purified from a sample derived from a subject.
- 20 20. A kit comprising an anti-Factor C3b antibody, an anti-Factor Ba antibody, a first moiety and a second moiety, wherein:
 - (a) the anti-Factor C3b antibody is labeled or can be labeled with the first moiety, the anti-Factor Ba antibody is labeled or can be labeled with the second moiety; and
 - (b) one of the moieties is a donor, and the other moiety is an acceptor.
- 25 21. The kit of claim 20, wherein the anti-Factor C3b antibody and/or the anti-Factor Ba antibody is immobilized on a solid surface, in particular wherein the solid surface is a plate, a microplate, a chip, a membrane, or a bead.
- 30 22. The kit of any of claim 20 or 21, further comprising (i) a control sample with known Factor D activity, or (ii) a control Factor D inhibitor with known potency of inhibiting Factor D activity.
23. The kit of any of claims 20-22, further comprising a quencher, in particular wherein the quencher is a Factor D inhibitor.
- 35 24. The kit of any of claims 20-23, further comprising (i) a recombinantly expressed Factor B, or (ii) endogenously expressed Factor B purified from a sample derived from a subject.
25. The kit of any of claims 20-24, further comprising (i) a recombinantly expressed Factor D, or (ii) endogenously expressed Factor D purified from a sample derived from a subject.

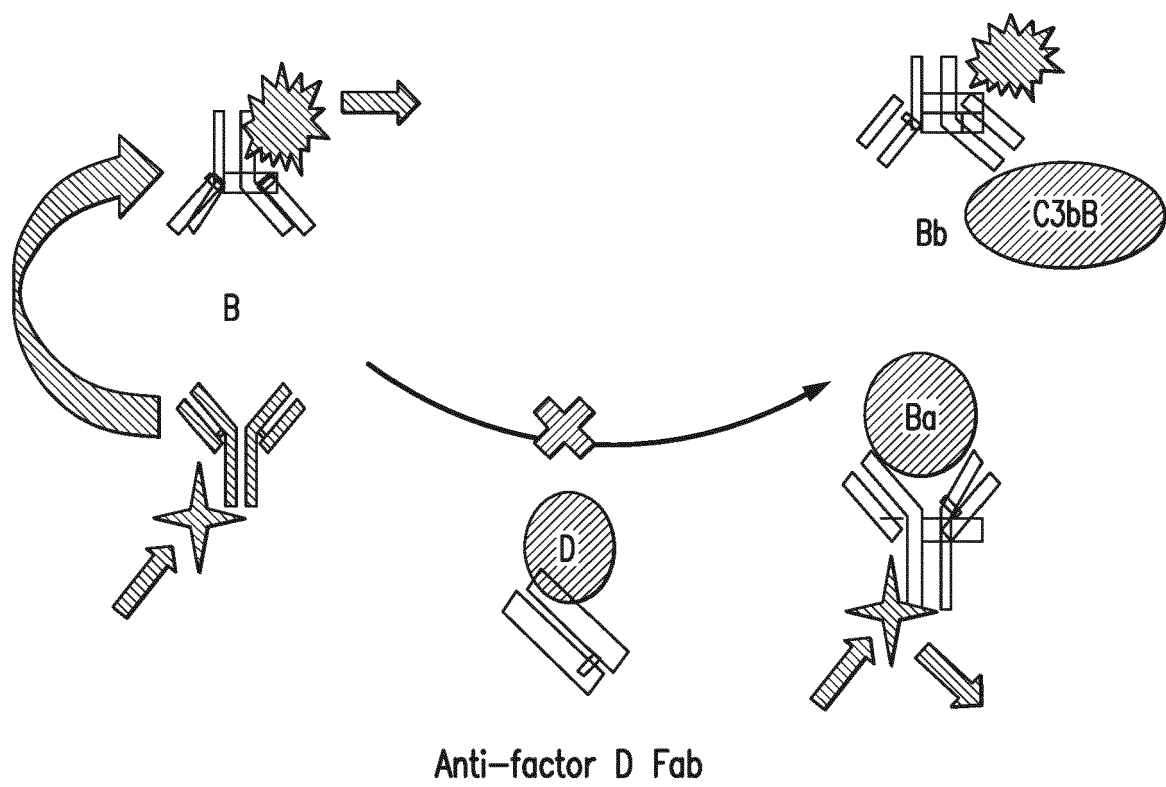


FIG. 1

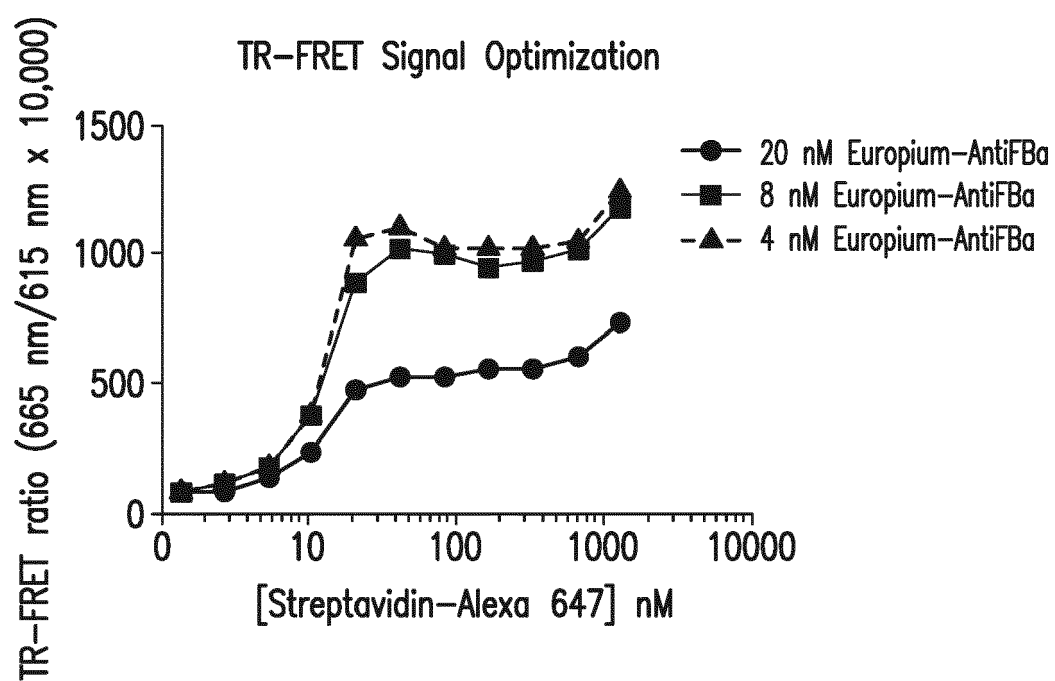


FIG. 2

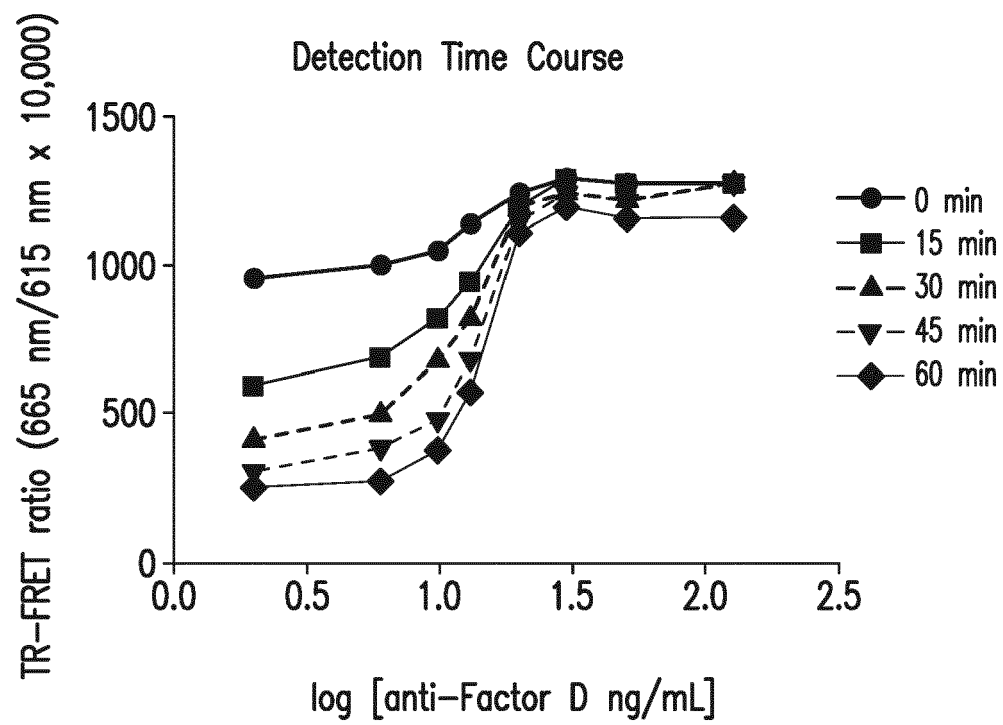


FIG. 3

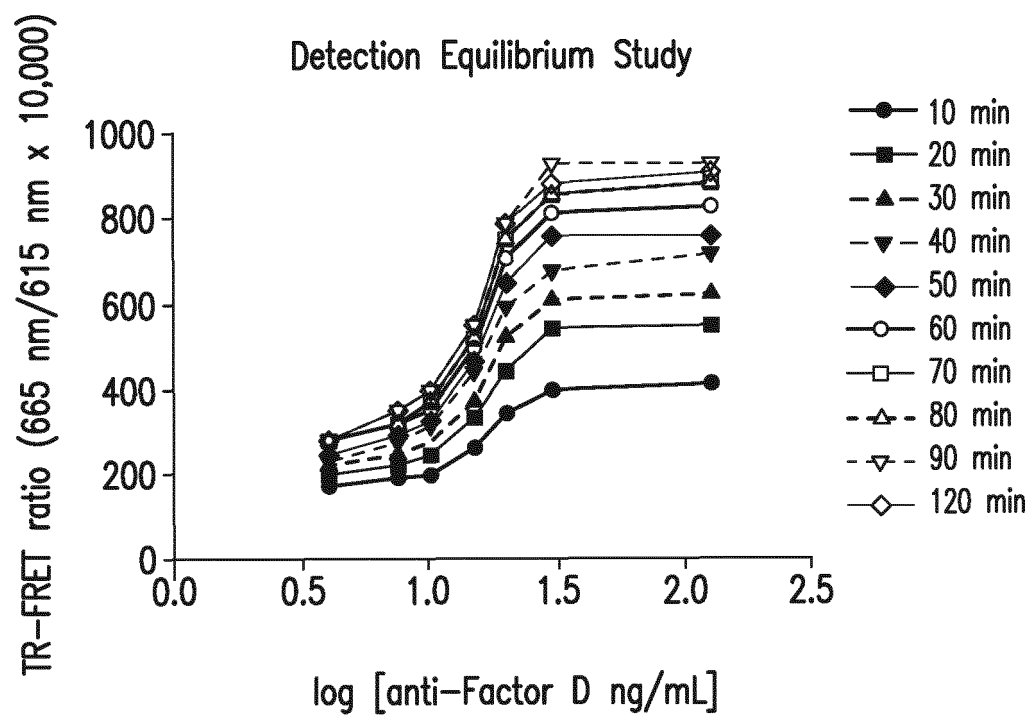


FIG. 4

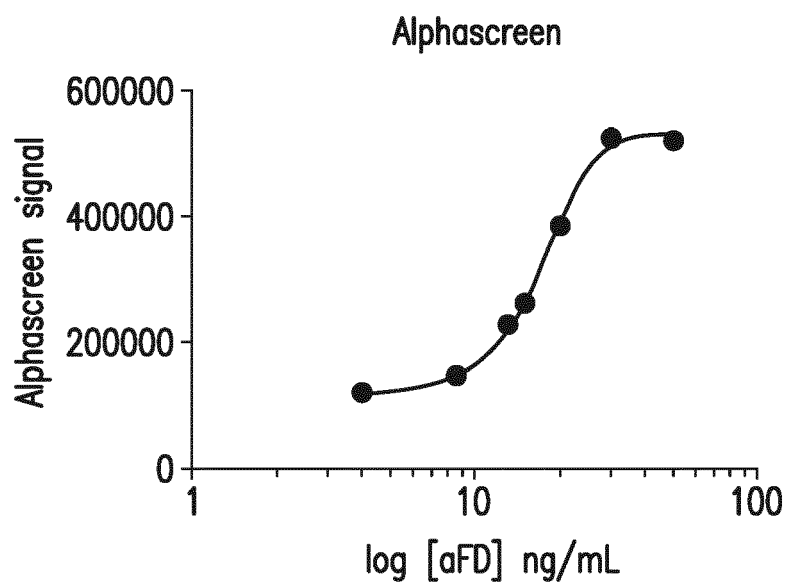


FIG. 5A

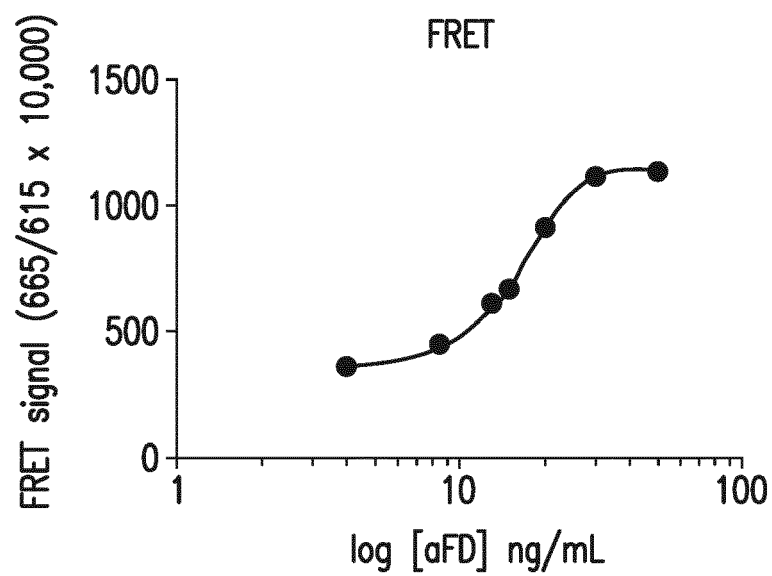


FIG. 5B



EUROPEAN SEARCH REPORT

Application Number
EP 19 20 0945

5

10

15

20

25

30

35

40

45

1

50

55

DOCUMENTS CONSIDERED TO BE RELEVANT			
Category	Citation of document with indication, where appropriate, of relevant passages	Relevant to claim	CLASSIFICATION OF THE APPLICATION (IPC)
A	WO 2014/028861 A1 (APELLIS PHARMACEUTICALS INC [US]) 20 February 2014 (2014-02-20) * claims 1, 8-11 and 21; paragraphs 130, 147; Table 1 *	1-25	INV. C12Q1/37 G01N33/542
A	INAGI REIKO ET AL: "Evaluation of the proteolytic activity of factor D accumulated as an active serine protease in patients with chronic renal failure", NEPHRON, S. KARGER AG, SWITZERLAND, vol. 66, no. 3, 1 January 1994 (1994-01-01), pages 285-290, XP009192970, ISSN: 0028-2766 * Whole document, in particular page 287, column 1, paragraph 1; page 289, column 1, paragraph 1 and figure 4 *	1-25	
A,D	TANHEHCO E J ET AL: "The anti-factor D antibody, MAb 166-32, inhibits the alternative pathway of the human complement system", TRANSPLANTATION PROCEEDINGS, ELSEVIER INC, ORLANDO, FL; US, vol. 31, no. 5, 1 August 1999 (1999-08-01), pages 2168-2171, XP002454359, ISSN: 0041-1345, DOI: 10.1016/S0041-1345(99)00297-3 * Whole document, in particular page 2169, column 1, paragraphs 2, 3 and 6 and column 2, paragraphs 3 and 4; page 2170, column 1, paragraph 3; figures 1 and 3 *	1-25	TECHNICAL FIELDS SEARCHED (IPC) C12Q G01N
A	WO 2014/055835 A1 (NOVELMED THERAPEUTICS INC [US]) 10 April 2014 (2014-04-10) * Whole document, in particular abstract and paragraph 245 *	1-25	
The present search report has been drawn up for all claims			
Place of search Munich		Date of completion of the search 12 March 2020	Examiner López García, F
CATEGORY OF CITED DOCUMENTS X : particularly relevant if taken alone Y : particularly relevant if combined with another document of the same category A : technological background O : non-written disclosure P : intermediate document		T : theory or principle underlying the invention E : earlier patent document, but published on, or after the filing date D : document cited in the application L : document cited for other reasons & : member of the same patent family, corresponding document	



EUROPEAN SEARCH REPORT

Application Number
EP 19 20 0945

5

10

15

20

25

30

35

40

45

50

55

DOCUMENTS CONSIDERED TO BE RELEVANT			
Category	Citation of document with indication, where appropriate, of relevant passages	Relevant to claim	CLASSIFICATION OF THE APPLICATION (IPC)
A,D	WO 99/42133 A1 (TANOX INC [US]) 26 August 1999 (1999-08-26) * ABSTRACT; p. 48, "(3) Complement Bb ELISA" * -----	1-25	
			TECHNICAL FIELDS SEARCHED (IPC)
The present search report has been drawn up for all claims			
Place of search Munich		Date of completion of the search 12 March 2020	Examiner López García, F
CATEGORY OF CITED DOCUMENTS			
X : particularly relevant if taken alone Y : particularly relevant if combined with another document of the same category A : technological background O : non-written disclosure P : intermediate document		T : theory or principle underlying the invention E : earlier patent document, but published on, or after the filing date D : document cited in the application L : document cited for other reasons & : member of the same patent family, corresponding document	

EPO FORM 1503 03.82 (P04C01)

**ANNEX TO THE EUROPEAN SEARCH REPORT
ON EUROPEAN PATENT APPLICATION NO.**

EP 19 20 0945

5 This annex lists the patent family members relating to the patent documents cited in the above-mentioned European search report.
The members are as contained in the European Patent Office EDP file on
The European Patent Office is in no way liable for these particulars which are merely given for the purpose of information.

12-03-2020

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 2014028861 A1	20-02-2014	US 2016067357 A1	10-03-2016
		WO 2014028861 A1	20-02-2014
-----	-----	-----	-----
15 WO 2014055835 A1	10-04-2014	AU 2013326932 A1	14-05-2015
		AU 2019213295 A1	29-08-2019
		CA 2887050 A1	10-04-2014
		CN 104870474 A	26-08-2015
		EP 2904014 A1	12-08-2015
20		JP 2015532303 A	09-11-2015
		US 2015315268 A1	05-11-2015
		US 2016122419 A1	05-05-2016
		US 2019031747 A1	31-01-2019
		WO 2014055835 A1	10-04-2014
-----	-----	-----	-----
25 WO 9942133 A1	26-08-1999	AT 412431 T	15-11-2008
		AU 762050 B2	19-06-2003
		BR 9909220 A	21-11-2000
		BR PI9909220 B1	18-09-2018
		CA 2321140 A1	26-08-1999
30		CN 1298308 A	06-06-2001
		CN 101298481 A	05-11-2008
		CY 1108663 T1	09-04-2014
		DK 1054693 T3	08-12-2008
		DK 2033659 T3	17-02-2014
35		EP 1054693 A1	29-11-2000
		EP 2033659 A2	11-03-2009
		EP 2277920 A2	26-01-2011
		EP 2848634 A1	18-03-2015
		EP 3056516 A1	17-08-2016
		EP 3260467 A1	27-12-2017
40		ES 2317689 T3	16-04-2009
		ES 2446930 T3	10-03-2014
		ES 2488819 T3	29-08-2014
		HK 1036016 A1	31-10-2008
		JP 4437192 B2	24-03-2010
45		JP 2002503706 A	05-02-2002
		KR 20010040585 A	15-05-2001
		NZ 506920 A	19-12-2003
		PT 1054693 E	22-01-2009
		SI 1054693 T1	30-04-2009
		SI 2033659 T1	31-03-2014
50		US 2006240020 A1	26-10-2006
		WO 9942133 A1	26-08-1999
-----	-----	-----	-----

EPO FORM P0459

For more details about this annex : see Official Journal of the European Patent Office, No. 12/82

REFERENCES CITED IN THE DESCRIPTION

This list of references cited by the applicant is for the reader's convenience only. It does not form part of the European patent document. Even though great care has been taken in compiling the references, errors or omissions cannot be excluded and the EPO disclaims all liability in this regard.

Patent documents cited in the description

- US 62249073 [0001]
- US 62250885 B [0001]
- WO 1999042133 A [0126]
- WO 2007056227 A [0126]
- WO 2008055206 A [0126]
- WO 2008147883 A [0126]
- WO 2009134711 A [0126]
- US 4179337 A [0395] [0401]
- US 7122636 B [0395] [0401]
- US 20070092940 A [0396]
- WO 2011069104 A [0396]

Non-patent literature cited in the description

- **KATSCHE et al.** *J Biol Chem*, 2012, vol. 287, 12886-12892 [0004] [0480]
- **DAMICO et al.** *Arq Bras Oftalmol*, 2012, vol. 75, 71-75 [0004] [0480]
- **TANHEHCO.** *Transplant Proc.*, 1999, vol. 31, 2168-2171 [0005] [0481]
- **VOLANAKIS et al.** *Protein Science*, 1996, vol. 5, 553-564 [0008] [0091]
- **KINDT et al.** *Kuby Immunology*. W.H. Freeman and Co, 2007, 91 [0071]
- **PORTOLANO et al.** *J. Immunol.*, 1993, vol. 150, 880-887 [0071]
- **CLARKSON et al.** *Nature*, 1991, vol. 352, 624-628 [0071]
- **KABAT et al.** *Sequences of Proteins of Immunological Interest*. Public Health Service, National Institutes of Health, 1991 [0072] [0076]
- **XU et al.** *Immunity*, 2000, vol. 13, 37-45 [0076]
- **JOHNSON ; WU.** *Methods in Molecular Biology*. Human Press, 2003, vol. 248, 1-25 [0076]
- **CHOTHIA ; LESK.** *J. Mol. Biol.*, 1987, vol. 196, 901-917 [0076]
- **MACCALLUM et al.** *J. Mol. Biol.*, 1996, vol. 262, 732-745 [0076]
- **MORRISON.** *Anal Biochem*, 1988, vol. 174, 101-120 [0081]
- **ULLMAN et al.** *Proc Natl Acad Sci U S A*, 1994, vol. 91, 5426-5430 [0081]
- **ULLMAN et al.** *Clin Chem*, 1996, vol. 42, 1518-1526 [0081]
- **GLICKMAN et al.** *Journal of Biomolecular Screening*, 2002, vol. 7, 3-10 [0081]
- **BIELEFELD-SEVIGNY.** *Assay Drug Dev Technol*, 2009, vol. 7, 90-92 [0081]
- **GULLBERG et al.** *Proc Natl Acad Sci U S A*, 2004, vol. 101, 8420-8424 [0081]
- **STRYER.** *Ann Rev Biochem*, 1978, vol. 47, 819-846 [0084]
- **CANTOR ; SCHIMMEL.** *Biophysical Chemistry Part II: Techniques for the Study of Biological Structure And Function*. W. H. Freeman and Co, 1980, 448-455 [0084]
- **SELVIN.** *Methods in Enzymology*, 1995, vol. 246, 300-335 [0084]
- **HAUGLAND et al.** *Proc Natl Acad Sci USA*, 1969, vol. 63, 24-30 [0084]
- *Fluorescence Spectroscopy*. Marcel Dekker, 1971 [0085]
- **WHITE et al.** *Fluorescence Analysis: A practical Approach*. Marcel Dekker, 1970 [0085]
- **HAUGLAND.** *Handbook of Fluorescent Probes and Research Chemicals*. Molecular Probes, Inc, 1996 [0085]
- **JEVSEVAR et al.** *Biotech. J.*, 2010, vol. 5, 113-128 [0395]
- **JUNUTULA, J. R. et al.** *J. Immunol Methods*, 2008, vol. 332 (1-2), 41-52 [0396]
- **VOLANAKIS ; NARAYANA.** *Protein Sci*, 1996, vol. 5, 553-564 [0480]